



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact **the searcher or contact:**

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ *I am an examiner in Workgroup:* *Example: 1610*

➤ *Relevant prior art found, search results used as follows:*

- 102 rejection
- 103 rejection
- Cited as being of interest.
- Helped examiner better understand the invention.
- Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- Foreign Patent(s)
- Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art not found:*

- Results verified the lack of relevant prior art (helped determine patentability).
- Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library, Remsen Bldg.

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171003

STIC-Biotech/ChemLib

From: Hines, Ja-Na
Sent: Tuesday, November 08, 2005 2:38 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search

Good Afternoon,
I would like to request a sequence and interference search
for application 10/043,344. In particular SEQ ID NO:50, 61, 74 and 85.

Thanks so much!!
Ja-Na Hines (76048)
AU:1645
Office: Rem 3B29
Mailbox: Rem 3C18
x20859

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: *11/9/05*
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA#: *4*
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: *Q22P*
WWW/Internet: _____
Other (Specify): _____

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OM protein - protein search, using sw model

Run on: November 9, 2005, 19:01:45 ; Search time 28.9506 Seconds (without alignments)

116.322 Million cell updates/sec

Title: US-10-043-344-61

Perfect score: 186

Sequence: 1 FTSEGTLEGPFYGPESQELGGKFLAHDKKVLFGVFS 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : PIR_79;*
1: Pir1;*
2: Pir2;*
3: Pir3;*
4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	92.5	648	2 S70907	transferrin-bindin
2	159	85.5	625	2 D64107	transferrin-bindin
3	159	85.5	630	2 S70909	transferrin-bindin
4	159	85.5	631	2 S70910	transferrin-bindin
5	157	84.4	654	2 S70908	transferrin-bindin
6	156	83.9	631	2 S70908	transferrin-bindin
7	150	80.6	660	2 S70904	transferrin-bindin
8	113	61.0	599	2 N0818	transferrin-bindin
9	109	58.6	547	2 S49814	transferrin-bindin
10	107	57.5	547	2 S49815	transferrin-bindin
11	107	57.5	547	2 A44796	transferrin-bindin
12	102	54.8	593	2 S27483	transferrin-bindin
13	102	54.8	593	2 B44796	transferrin-bindin
14	97	52.2	737	2 H81070	lactoferrin-bindin
15	97	52.2	741	2 D81798	transferrin-bindin
16	94.5	50.8	711	2 S70660	transferrin-bindin
17	91.5	49.2	712	2 E81196	transferrin-bindin
18	91.5	49.2	689	2 S70661	transferrin-bindin
19	90.5	48.7	698	2 D81832	transferrin-bindin
20	90.5	48.7	299	2 G64105	transferrin-bindin
21	78	41.9	289	2 E81003	transferrin-bindin
22	66	35.5	488	2 C82025	proteobacterial periplasm
23	66	35.5	497	2 A49341	isocitrate dehydrogenase (imp)
24	60	32.3	742	2 A49341	conserved hypothetical protein
25	59.5	32.0	389	2 T44975	hypothetical protein
26	59	31.7	241	2 A62915	hypothetical protein
27	59	31.7	241	2 B97690	hypothetical protein
28	56	30.1	394	2 A86431	hypothetical protein
	29	29.6	200	2 AH3260	outer membrane lip

ALIGNMENTS

RESULT 1

S70907 transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB12)

C;Species: Haemophilus influenzae

A;Variety: Strain SB12

C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

R;Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E.; Mol. Microbiol. 19: 575-586, 1996

A;Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes

A;Reference number: S70901; MUID:96228706; PMID:8830248

A;Accession: S70907

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-648 <LOO>

A;Cross-references: UNIPROT:048040; EMBL:U15054

A;Experimental source: strain SB12, clone DS-1047-1-2

R;Loosmore, S.M.

Submitted to the EMBL Data Library, September 1994

A;Reference number: S73320

A;Accession: S73320

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-533, 'V', 535-542, 'I', 544-559, 'G', 561-648 <LOW>

A;Cross-references: EMBL:U1534; PID:9223946; PMID:ARC43901; PID:91223947

A;Experimental source: strain SB12, clone DS-1047-1-2

C;Genetics:

A;Gene: cbp2

C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a F:1-17/Domain: signal sequence #stratus predicted <SIG>

F:1-648/Product: transferrin-binding protein 2 #stratus predicted <MMT>

Query Match 92.5%: Score 172; DB 2; Length 648;

Best Local Similarity 94.3%; Pred. No. 2.1e-15;

Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FTSGTLEGPFYGPQGQELGGKFLAHDKKVLFGVFS 35

Db 291 FTSGTLEGPFYGPQGQELGGKFLAHDKKVGFVFS 325

RESULT 2

D64107 transferrin-binding protein 2 precursor - Haemophilus influenzae (strain Rd KW20)

C;Species: Haemophilus influenzae

C;Accession: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.R.; Fleischmann, R.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.M.; Branden, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, N.S.M.; Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Smith, H.O.; Venter,

A;Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.
 A;Reference number: A64000; MUID:95350630; PMID:7542300
 A;Accession: D64107
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-625 <LOO>
 A;Cross-references: UNIPROT:P44971; GB:U32780; PIDN: AAC22657.1;
 C;Genetics:
 A;Gene: tbp2
 C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
 F;1-17/Domain: signal sequence #status predicted <SIG>
 F;18-625/Product: transferrin-binding protein 2 #status predicted <MAT>
 Query Match 85.5%; Score 159; DB 2; Length 625;
 Best Local Similarity 85.7%; Pred. No. 1-2e-13;
 Matches 30; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 C;Genetics:
 Qy 1 FTSEGTLEGFFYGPQQELGGKFLAHDKVTLGVFS 35
 Db 287 FTREGTLEGFFYGPNGPEELGGKFLAGDKVFGVFS 3221

RESULT 3
 S7009 transferrin-binding protein 2 precursor - *Haemophilus influenzae* (strain SB30)
 A;Variety: *Haemophilus influenzae*
 A;Species: *Haemophilus influenzae*
 A;Strain: SB30
 A;Accession: S700905; S73322
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C;Cross-references: UNIPROT:Q48012; EMBL:U15056
 R;Loosmore, S. M.; Yang, Y.; Coleman, D. C.; Shortreed, J. M.; England, D. M.; Harkness, R. E.
 Mol. Microbiol. 19, 575-586, 1996
 A;Title: Cloning and expression of the *Haemophilus influenzae* transferrin receptor genes
 A;Reference number: S70091; MUID:96228706; PMID:8830348
 A;Accession: S70099
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-630 <LOO>
 A;Cross-references: UNIPROT:Q48012; EMBL:U15056
 A;Experimental source: strain SB30; clone DS-1047-3-3
 R;Loosmore, S. M.
 Submitted to the EMBL Data Library, September 1994
 A;Reference number: S73320
 A;Accession: S73322
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-448, 'T', 450, 'I', 452-630 <LOW>
 A;Cross-references: EMBL:U15056; PIDN:G123350; PIDN:MAC43932.1; PID:91223951
 A;Experimental source: strain SB30; clone DS-1047-3-3
 C;Genetics:
 A;Gene: tbp2
 C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
 F;1-17/Domain: signal sequence #status predicted <SIG>
 F;18-630/Product: transferrin-binding protein 2 #status predicted <MAT>
 Query Match 85.5%; Score 159; DB 2; Length 630;
 Best Local Similarity 85.7%; Pred. No. 1-2e-13;
 Matches 30; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 C;Genetics:
 Qy 1 FTSEGTLEGFFYGPQQELGGKFLAHDKVTLGVFS 35
 Db 290 FTSEGTLEGFFYGPNGPEELGGKFLASDKVFGVFS 324

RESULT 4
 S70910 transferrin-binding protein 2 precursor - *Haemophilus influenzae* (strain SB32)
 C;Species: *Haemophilus influenzae*
 A;Variety: strain SB32
 A;Strain: SB32
 A;Accession: S70910; S73323
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C;Cross-references: UNIPROT:Q48043; EMBL:U15057
 R;Loosmore, S. M.; Yang, Y.; Coleman, D. C.; Shortreed, J. M.; England, D. M.; Harkness, R. E.
 Mol. Microbiol. 19, 575-586, 1996
 A;Title: Cloning and expression of the *Haemophilus influenzae* transferrin receptor genes
 A;Reference number: S70905; S73324
 A;Accession: S70905
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-654 <LOO>
 A;Cross-references: UNIPROT:Q48038; EMBL:U15053; PIDN:G1233943; PIDN:AC43928.1; PID:91223952
 A;Experimental source: strain PAK 12085
 C;Genetics:
 A;Gene: tbp2
 C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
 F;1-17/Domain: signal sequence #status predicted <SIG>
 F;18-654/Product: transferrin-binding protein 2 #status predicted <MAT>
 Query Match 84.4%; Score 157; DB 2; Length 654;
 Best Local Similarity 82.9%; Pred. No. 2.e-13;
 Matches 29; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 C;Genetics:
 Qy 1 FTSEGTLEGFFYGPQQELGGKFLAHDKKVLGVFS 35
 Db 290 FTSEGTLEGFFYGPNGPEELGGKFLASDKVFGVFS 324

RESULT 5
 S70905 transferrin-binding protein 2 precursor - *Haemophilus influenzae* (strain PAK 12085)
 C;Species: *Haemophilus influenzae*
 A;Variety: strain PAK 12085
 A;Strain: PAK 12085
 A;Accession: S70905
 C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 R;Loosmore, S. M.; Yang, Y.; Coleman, D. C.; Shortreed, J. M.; England, D. M.; Harkness, R. E.
 Mol. Microbiol. 19, 575-586, 1996
 A;Title: Cloning and expression of the *Haemophilus influenzae* transferrin receptor genes
 A;Reference number: S70901; MUID:96228706; PMID:8830248
 A;Accession: S70905
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-654 <LOO>
 A;Cross-references: UNIPROT:Q48038; EMBL:U15053; PIDN:G1233943; PIDN:AC43928.1; PID:91223952
 A;Experimental source: strain PAK 12085
 C;Genetics:
 A;Gene: tbp2
 C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
 F;1-17/Domain: signal sequence #status predicted <SIG>
 F;18-654/Product: transferrin-binding protein 2 #status predicted <MAT>
 Query Match 84.4%; Score 157; DB 2; Length 654;
 Best Local Similarity 82.9%; Pred. No. 2.e-13;
 Matches 29; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

RESULT 6
 S70908 transferrin-binding protein 2 precursor - *Haemophilus influenzae* (strain SB29)
 C;Species: *Haemophilus influenzae*
 A;Variety: strain SB29
 A;Strain: SB29
 A;Accession: S70908; S73321
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 R;Loosmore, S. M.; Yang, Y.; Coleman, D. C.; Shortreed, J. M.; England, D. M.; Harkness, R. E.
 Mol. Microbiol. 19, 575-586, 1996
 A;Title: Cloning and expression of the *Haemophilus influenzae* transferrin receptor genes

A;Reference number: S70901; MUID:96228706; PMID:8830248

A;Accession: S70908

A;Molecule type: DNA

A;Residues: 1-631 <LOO>

A;Cross-references: UNIPROT:Q48041; EMBL:U15055

A;Experimental source: strain SB29, clone DS-1090-3-2

R;Loosmore, S.M.

Submitted to the EMBL Data Library, September 1994

A;Reference number: S73320

A;Accession: S73321

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-250, L', 252-349, 'RTDATN', 357-631 <LOW>

A;Cross-references: EMBL:U15055; NID:SI2233948; PIDN:AC43931.1; PID:912231949

A;Experimental source: strain SB29, clone DS-1090-3-2

C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a

F;17/Domain: signal sequence #status predicted <SIG>

F;18-631/Product: transferrin-binding protein 2 #status predicted <MAT>

C;Genetics:

A;Gene: tbp2

A;Cross-references: UNIPROT:Q48041; EMBL:U15055

A;Experimental source: strain SB29, clone DS-1090-3-2

R;Loosmore, S.M.

Submitted to the EMBL Data Library, September 1994

A;Reference number: S70901

A;Accession: S70902

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-660 <LOO>

A;Cross-references: UNIPROT:Q57443; EMBL:U5051; NID:912233937; PIDN: AAC41924.1; PID:912233937

A;Accession: S70902

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-660 <LOO>

A;Cross-references: EMBL:U15052; NID:912233940; PIDN:AC43926.1; PID:91223941

A;Accession: S70904

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-660 <LOO>

A;Cross-references: UNIPROT:Q57443; EMBL:U5051; NID:912233937; PIDN: AAC41924.1; PID:912233937

A;Accession: S70902

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-660 <LOO>

A;Cross-references: strain Minra, clone DS-712-1-3

C;Genetics:

A;Gene: tbp2

A;Cross-references: strain Minra, clone DS-712-1-3

C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a

F;17/Domain: signal sequence #status predicted <SIG>

F;18-660/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 80 6%; Score 150; DB 2; Length 660;

Best Local Similarity 80.0%; Pred. No. 2.1e-12;

Matches 28; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 FTSEGTLGGFPYGPQEGLGSKFLAHDKVKLGVSF 35

Db 288 FTSEGTLGGFPYGPNAEELGSKFLATDNRVFGVFS 322

RESULT 8

JN0188

transferrin-binding protein 2 precursor - *Neisseria meningitidis* (strain B16B6)

C;Species: *Neisseria meningitidis*

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

R;Loosmore, S.M.

Submitted to the EMBL Data Library, September 1994

A;Reference number: S70901

A;Accession: S70902

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-660 <LOO>

A;Cross-references: UNIPROT:Q44168; EMBL:Z46775; PIDN:CAA86730.1; PID:G5775

A;Cross-references: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a

C;Accession: JN0818; PMID:80633; S33153

R;Loosmore, M.; Mazarin, V.; Irwin, S.W.; Bouchon, B.; Quentin-Millet, M.J.; Jacobs, E.;

Gene 130, 73-80, 1993

A;Title: Cloning and characterization of *Neisseria meningitidis* genes encoding the trans

A;Reference number: JN0818

A;Accession: JN0818

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-599 <LEG>

A;Cross-references: UNIPROT:006988; EMBL:Z15129; PIDN:CAA78830.1; PID:9297042

A;Accession: PN0633

A;Molecule type: protein

A;Residues: 21-34;51-61;158-171;351-361;363-386;441-456;564-582 <LEG1>

C;Genetics:

A;Gene: tbp2

A;Cross-references: UNIPROT:Q48041; EMBL:U15055

A;Experimental source: strain SB29, clone DS-1090-3-2

R;Loosmore, S.M.

Submitted to the EMBL Data Library, September 1994

A;Reference number: S73320

A;Accession: S73321

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-250, L', 252-349, 'RTDATN', 357-631 <LOW>

A;Cross-references: EMBL:U15055; NID:SI2233948; PIDN:AC43931.1; PID:912231949

A;Experimental source: strain SB29, clone DS-1090-3-2

C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a

F;17/Domain: signal sequence #status predicted <SIG>

F;18-631/Product: transferrin-binding protein 2 #status predicted <MAT>

C;Genetics:

A;Gene: tbp2

A;Cross-references: UNIPROT:Q48041; EMBL:U15055

A;Experimental source: strain SB29, clone DS-1090-3-2

R;Loosmore, S.M.

Submitted to the EMBL Data Library, September 1994

A;Reference number: S70901

A;Accession: S70902

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-660 <LOO>

A;Cross-references: UNIPROT:Q57443; EMBL:U5051; NID:912233937; PIDN: AAC41924.1; PID:912233937

A;Accession: S70902

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-660 <LOO>

A;Cross-references: strain Minra, clone DS-712-1-3

C;Genetics:

A;Gene: tbp2

A;Cross-references: strain Minra, clone DS-712-1-3

C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a

F;17/Domain: signal sequence #status predicted <SIG>

F;18-660/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 61 0%; Score 113.5; DB 2; Length 599;

Best Local Similarity 61.9%; Pred. No. 1.8e-07;

Matches 22; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

Qy 1 FTSEGTLGGFPYGPQEGLGSKFLAHDKVKLGVSF 34

Db 308 FTSDSDSLEGGFPYGPQEGLGSKFLAHDKVKLGVSF 342

RESULT 9

S49814

transferrin-binding protein, outer membrane - *Actinobacillus pleuropneumoniae*

C;Species: *Actinobacillus pleuropneumoniae*

C;Accession: S49814

R;Bunka, S.; Potter, A.; Gerlach, G.

submitted to the EMBL Data Library, November 1994

A;Description: Cloning and sequencing of the transferrin-binding protein genes of *Actino*

M**l**. *Microbiol*. 19, 545-586, 1996

A;Title: Cloning and expression of the *Haemophilus influenzae* transferrin receptor genes

A;Reference number: S70901; MUID:96228706; PMID:8830248

A;Accession: S70904

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-547 <BUN>

A;Cross-references: UNIPROT:Q44167; EMBL:246774

A;Accession: S49814

C;Genetics:

A;Gene: tiba

A;Cross-references: UNIPROT:Q44167; EMBL:246774

C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a

F;17/Domain: signal sequence #status predicted <SIG>

F;18-660/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 58 6%; Score 109; DB 2; Length 547;

Best Local Similarity 65.5%; Pred. No. 6.6e-07;

Matches 19; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 7 LEGGYGPEQELGGSKFLAHDKVKLGVSF 35

Db 273 LEGGYGPEQELGGSKFLAHDKVKLGVSF 301

RESULT 10

S49815

transferrin-binding protein - *Actinobacillus pleuropneumoniae*

C;Species: *Actinobacillus pleuropneumoniae*

C;Accession: S49815

R;Bunka, S.; Potter, A.; Gerlach, G.

submitted to the EMBL Data Library, November 1994

A;Description: Cloning and sequencing of the transferrin-binding protein genes of *Actino*

M**l**. *Microbiol*. 19, 545-586, 1996

A;Title: Cloning and expression of the *Haemophilus influenzae* transferrin receptor genes

A;Reference number: S70901; MUID:96228706; PMID:8830248

A;Accession: S70902

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-547 <BUN>

A;Cross-references: UNIPROT:Q44168; EMBL:Z46775

A;Accession: S49815

C;Genetics:

A;Gene: tiba

A;Cross-references: UNIPROT:Q44168; EMBL:Z46775

C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a

F;17/Domain: signal sequence #status predicted <SIG>

F;18-660/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 80 6%; Score 150; DB 2; Length 660;

Best Local Similarity 80.0%; Pred. No. 2.1e-12;

Matches 28; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 FTSEGTLGGFPYGPQEGLGSKFLAHDKVKLGVSF 35

Db 288 FTSEGTLGGFPYGPNAEELGSKFLATDNRVFGVFS 322

Query Match 57.5%; Score 107; DB 2; Length 547;
 Best Local Similarity 60.0%; Pred. No. 1.2e-06; Indels 0; Gaps 0;
 Matches 18; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 A; Status: preliminary

Db 6 TLEGGFYGPQEQELGGKFLAHDKKVLGVFS 35
 271 SLEGGFYGPKAEMAKFVANDKSLSLFAVFS 300

RESULT 11
 A44796
 transferrin-binding protein, tfbA - *Actinobacillus pleuropneumoniae*
 C;Species: *Actinobacillus pleuropneumoniae*
 C;Date: 24-Jan-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A44796; S27484
 R;Gerlach, G.F.; Klashinsky, S.; Anderson, C.; Potter, A.A.; Willson, P.J.
 Infect. Immun. 60, 3253-3261, 1992
 A;Title: Characterization of two genes encoding distinct transferrin-binding proteins in
 A;Reference number: A44796; MUID:92347999; PMID:1639494
 A;Contents: AP37; serotype 17
 A;Accession: A44796
 A;Molecule type: DNA
 A;Residues: 1-553 <GER>
 A;Cross-references: UNIPROT:Q44169; GB:MB5274; NID:9141840; PIDN:AAA21928.1; PMID:9141841
 C;Superfamily: bacterial pathogen transferrin-binding protein; tmb-dependent receptor a
 C;Text: sequence extracted from NCBI backbone (NCBIN:109737, NCBI:109738)
 A;Note: sequence extracted from NCBI backbone (NCBIN:109735, NCBI:109736)
 C;Genetics:
 A;Gene: tfbA
 C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
 C;Text: sequence inconsistent with the nucleotide translation
 Query Match 57.5%; Score 107; DB 2; Length 547;
 Best Local Similarity 60.0%; Pred. No. 1.2e-06;
 Matches 18; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 A;Status: preliminary
 A;Accession: A81000; MUID:10710307
 A;Cross-references: UNIPROT:Q9JYK4; GB:AE002504; GB:AE002098; NID:97226785; PIDN:AAF41896
 A;Experimental source: serogroup B, strain MC58
 C;Genetics:
 A;Gene: NMB1541

RESULT 12
 S27483
 transferrin-binding protein - *Actinobacillus pleuropneumoniae*
 C;Species: *Actinobacillus pleuropneumoniae*
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S27483
 R;Gerlach, G.F.; Klashinsky, S.; Anderson, C.; Potter, A.A.; Wilson, P.
 Submitted to the EMBL Data Library, March 1992
 A;Description: Characterization of an *Actinobacillus pleuropneumoniae* transferrin-bindin
 A;Reference number: S27483
 A;Accession: S27483
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-593 <GER>
 A;Cross-references: UNIPROT:Q44169; EMBL:MB5274
 C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
 C;Text: sequence extracted from NCBI backbone (NCBIN:109737, NCBI:109738)
 Query Match 54.8%; Score 102; DB 2; Length 593;
 Best Local Similarity 48.6%; Pred. No. 6.5e-06;
 Matches 17; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
 A;Status: preliminary
 A;Accession: A81775; MUID:107161919
 A;Cross-references: UNIPROT:Q9JYK3; GB:AI1622757; PIDN:97380371; PMID:97380371; NID:9157959; PIDN:9157959
 C;Species: *Actinobacillus pleuropneumoniae*
 C;Accession: A44796
 C;Text: sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 Query Match 1 FTSEGTYGPQEQELGGKFLAHDKKVLGVFS 35
 312 FTDSNYLEGGFYGPKAEMAKFVANDKSLSLFAVFA 346
 Db

RESULT 13
 B44796
 transferrin-binding protein, TfbA - *Actinobacillus pleuropneumoniae*
 C;Species: *Actinobacillus pleuropneumoniae*
 C;Accession: A44796
 C;Text: sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 Query Match 54.8%; Score 102; DB 2; Length 593;
 Best Local Similarity 48.6%; Pred. No. 6.5e-06;
 Matches 17; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
 A;Status: preliminary
 A;Accession: A81775; MUID:10722556; PMID:107198
 A;Cross-references: UNIPROT:Q9JYK3; GB:AI1622757; PIDN:97380371; PMID:97380371; NID:9157959; PIDN:9157959
 C;Species: *Actinobacillus pleuropneumoniae*
 C;Accession: A44796
 C;Text: sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 Query Match 1 FTSEGTYGPQEQELGGKFLAHDKKVLGVFS 35
 312 FTDSNYLEGGFYGPKAEMAKFVANDKSLSLFAVFA 346
 Db

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Query Match      52.2%;  Score 97;  DB:2;  Length 741;
Best Local Similarity 55.2%;  Pred. No. 3.9e-05;
Matches 16;  Conservative 7;  Mismatches 6;  Indels 0;  Gaps 0;
Matches 16;  Conservative 7;  Mismatches 6;  Indels 0;  Gaps 0;

Qy   7 LEGGPYGPBGOBLGGKPLAHDKKVULGVFES 35
     ||||:|:||:||:||:||:||:||:||:||:||:||:|
Db  326 LEGGFFGDDNGEBLAGRFISNDNSVFGVFA 354
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Search completed: November 9, 2005, 19:24:01
Job time : 34.9506 secs

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Scoring table:	BLOSUM62	ALIGMENTS
Gapop:	10.0 , Gapext 0.5	
Searched:	1612378 seqs, 512079187 residues	
Total number of hits satisfying chosen parameters:	1612378	
Minimum DB seq length:	0	RESULT 1
Maximum DB seq length:	2000000000	TBP2_HAEIN
Post-processing:	Minimum Match 0%	ID: P44571;
	Maximum Match 100%	STANDARD: DT: 01-NOV-1995 (Rel. 32, Created)
Database :	UniProt_03: 1: uniprot_sprot: 2: uniprot_trembl: *	DT: 01-NOV-1995 (Rel. 32, Last sequence update)
		DT: 25-OCT-2004 (Rel. 45, Last annotation update)
		DB: Probable transferrin-binding protein 2 precursor, Name=tbpB; Synonyms=tbpB; OrderedLocusName=SHI0935;
		OS: Haemophilus influenzae.
		OC: Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
		OC: Pasteurellaceae; Haemophilus.
		OX: NCBI_TaxID=727;
		RN: [1]
		RP: SEQUENCE FROM N.A.
		RC: STRAIN=Rd / KW20 / ATCC 51907;
		RX: MEDLINE=95350530; PubMed=7542800;
		RA: Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.B.P., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G.G., Pitzlugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Heidelberg B., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M., Gneim C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C., "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.", Science 269:496-512(1995).
		RL: FUNCTION: Acts as a transferrin receptor and is required for transferrin utilization (By similarity).
		CC: -I- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor (Probable).
		CC: This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Result No.	Query Score	Description
-	-	-
1	89.6	P44571 transferrin-binding protein 2 precursor
2	88.4	Q48040 haemophilus
3	84.8	Q48041 haemophilus
4	82.3	Q48042 haemophilus
5	82.3	Q48043 haemophilus
6	79.9	Q48034 haemophilus
7	79.9	Q48038 haemophilus
8	77.4	Q6H8U4 neisseria m
9	77.4	Q9FCSS3 neisseria m
10	77.4	Q6H8W5 neisseria C
11	77.4	Q6H8W6 neisseria S
12	77.4	Q6H8W3 neisseria F
13	77.4	Q6H8W1 neisseria m
14	76.2	Q6H8W0 neisseria F
15	76.2	Q6H8W1 neisseria F
16	76.2	Q6H8W4 neisseria S
17	75.6	Q6H8W5 neisseria m
18	75.0	Q6H8W1 neisseria S
19	75.0	Q6H8W4 neisseria F
20	75.0	Q6H8V8 neisseria m
21	75.0	Q9ZFD4 moraxella C
22	75.0	Q9Z106 moraxella C
23	75.0	Q85051 moraxella C
24	75.0	Q85056 moraxella C
25	72.6	Q9BX7 neisseria m
26	72.6	Q86397 neisseria m
27	72.6	Q51285 neisseria m
28	72.6	Q9JPL7 neisseria m
29	72.6	Q9FCR8 neisseria m
30	72.6	Q9BXA7 neisseria m
	69.2	Q9RLM1 neisseria m

SQ	SEQUENCE	625 AA;	MW:	52EFBC97B5ED4E9A	CRC64;	DR	PIR: S70908; S70908.
	Query Match	89.6%;	Score 147;	DB 1;	Length 625;	DR	GO: 0016020; C:membrane; IEA.
	Best Local Similarity	90.3%;	Pred. No. 1.3e-11;			DR	GO: 0004998; F:transferrin receptor activity; IEA.
	Matches 28;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;	DR	InterPro; IPR01677; Transferrin_bind.
Qy	1	LEGGFYGPKGPELGFPLAGDKKVFGVFSAK	31			DR	Pfam: PF01298; Lipoprotein_5;
Db	293	LEGGFYGPNGBGLGKPLAGDKKVFGVFSAK	323			SQ	SEQUENCE 631 AA;
	RESULT 2						69700 MW;
Q48040		PRELIMINARY;		PRT;	648 AA.	Query Match	84.8%; Score 139;
AC	Q48040;					Best Local Similarity 83.9%;	DB 2; Length 631;
DT	01-NOV-1996	(TREMBLrel. 01, Created)				Matches 26;	Conservative 2; Mismatches 3;
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)				Indels 0;	Gaps 0;
DE	01-MAR-2004	(TREMBLrel. 26, Last annotation update)					
GN	Name=tbp2;						
OS	Haemophilus influenzae.						
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;						
OC	Pasteurellaceae; Haemophilus.						
OX	NCBI_TaxID=727;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=SB12;						
RX	MEDLINE=98228706; PubMed=8830248;						
RA	Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,						
RA	Harkness R.B., Pele S.C., Klein M.H.;						
RT	"Cloning and expression of the Haemophilus influenzae transferrin receptor genes";						
RT	receptor genes";						
RL	Mol. Microbiol. 19:575-586 (1996).						
DR	EMBL: U15054; AAC43930.1; -.						
DR	PIR: S70907; S70907.						
DR	GO: GO:0016020; C:membrane; IEA.						
GO	GO: 0004998; F:transferrin receptor activity; IEA.						
DR	InterPro; IPR001677; Transferrin_bind.						
DR	Pfam: PF01298; Lipoprotein_5;						
SQ	SEQUENCE 648 AA;	71246 MW;	D83690AB33891A5A	CRC64;		Query Match	82.3%; Score 135;
						Best Local Similarity 83.9%;	DB 2; Length 630;
Qy	1	LEGGFYGPKGPELGFPLAGDKKVFGVFSAK	31			Matches 26;	Conservative 1; Mismatches 4;
Db	297	LEGGFYGPNGBGLGKPLAGDKKVFGVFSAK	327			Indels 0;	Gaps 0;
	RESULT 3						
Q48041		PRELIMINARY;		PRT;	631 AA.	Query Match	82.3%; Score 135;
AC	Q48041;					Best Local Similarity 83.9%;	DB 2; Length 630;
DT	01-NOV-1996	(TREMBLrel. 01, Created)				Matches 26;	Conservative 1; Mismatches 4;
DE	01-NOV-1996	(TREMBLrel. 01, Last sequence update)				Indels 0;	Gaps 0;
DE	01-MAR-2004	(TREMBLrel. 26, Last annotation update)					
GN	Name=tbp2;						
OS	Haemophilus influenzae.						
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;						
OC	Pasteurellaceae; Haemophilus.						
OX	NCBI_TaxID=727;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=SB12;						
RX	MEDLINE=98228706; PubMed=8830248;						
RA	Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,						
RA	Harkness R.B., Pele S.C., Klein M.H.;						
RT	"Cloning and expression of the Haemophilus influenzae transferrin receptor genes";						
RT	receptor genes";						
RL	Mol. Microbiol. 19:575-586 (1996).						
DR	EMBL: U15055; AAC43931.1; -.						
DR	PIR: S70908; S70908.						
DR	GO: 0016020; C:membrane; IEA.						
DR	InterPro; IPR01677; Transferrin_bind.						
DR	Pfam: PF01298; Lipoprotein_5;						
SQ	SEQUENCE 631 AA;	69700 MW;	8060778953F3B39	CRC64;		Query Match	82.3%; Score 135;
						Best Local Similarity 83.9%;	DB 2; Length 630;
Qy	1	LEGGFYGPKGPELGFPLAGDKKVFGVFSAK	31			Matches 26;	Conservative 1; Mismatches 4;
Db	296	LEGGFYGPNGBGLGKPLAGDKKVFGVFSAK	326			Indels 0;	Gaps 0;
	RESULT 4						
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AC	Q48042;					Best Local Similarity 83.9%;	DB 2; Length 630;
DT	01-NOV-1996	(TREMBLrel. 01, Created)				Matches 26;	Conservative 1; Mismatches 4;
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)				Indels 0;	Gaps 0;
DE	01-MAR-2004	(TREMBLrel. 26, Last annotation update)					
GN	Name=tbp2;						
OS	Haemophilus influenzae.						
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;						
OC	Pasteurellaceae; Haemophilus.						
OX	NCBI_TaxID=727;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=SB12;						
RX	MEDLINE=98228706; PubMed=8830248;						
RA	Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,						
RA	Harkness R.B., Pele S.C., Klein M.H.;						
RT	"Cloning and expression of the Haemophilus influenzae transferrin receptor genes";						
RT	receptor genes";						
RL	Mol. Microbiol. 19:575-586 (1996).						
DR	EMBL: U15055; AAC43931.1; -.						
DR	PIR: S70909; S70909.						
DR	GO: 0016020; C:membrane; IEA.						
DR	InterPro; IPR01677; Transferrin_bind.						
DR	Pfam: PF01298; Lipoprotein_5;						
SQ	SEQUENCE 630 AA;	69700 MW;	6PCB2D1B6B642C84	CRC64;		Query Match	82.3%; Score 135;
						Best Local Similarity 83.9%;	DB 2; Length 630;
Qy	1	LEGGFYGPKGPELGFPLAGDKKVFGVFSAK	31			Matches 26;	Conservative 1; Mismatches 4;
Db	296	LEGGFYGPNGBGLGKPLAGDKKVFGVFSAK	326			Indels 0;	Gaps 0;
	RESULT 5						
Q48043		PRELIMINARY;		PRT;	631 AA.	Query Match	82.3%; Score 135;
AC	Q48043;					Best Local Similarity 83.9%;	DB 2; Length 630;
DT	01-NOV-1996	(TREMBLrel. 01, Created)				Matches 26;	Conservative 1; Mismatches 4;
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)				Indels 0;	Gaps 0;
DE	01-MAR-2004	(TREMBLrel. 26, Last annotation update)					
GN	Name=tbp2;						
OS	Haemophilus influenzae.						
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;						
OC	Pasteurellaceae; Haemophilus.						
OX	NCBI_TaxID=727;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=SB12;						
RX	MEDLINE=98228706; PubMed=8830248;						
RA	Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,						
RA	Harkness R.B., Pele S.C., Klein M.H.;						
RT	"Cloning and expression of the Haemophilus influenzae transferrin receptor genes";						
RT	receptor genes";						
RL	Mol. Microbiol. 19:575-586 (1996).						
DR	EMBL: U15055; AAC43931.1; -.						
DR	PIR: S70909; S70909.						
DR	GO: 0016020; C:membrane; IEA.						
DR	InterPro; IPR01677; Transferrin_bind.						
DR	Pfam: PF01298; Lipoprotein_5;						
SQ	SEQUENCE 630 AA;	69700 MW;	6PCB2D1B6B642C84	CRC64;		Query Match	82.3%; Score 135;
						Best Local Similarity 83.9%;	DB 2; Length 630;
Qy	1	LEGGFYGPKGPELGFPLAGDKKVFGVFSAK	31			Matches 26;	Conservative 1; Mismatches 4;
Db	296	LEGGFYGPNGBGLGKPLAGDKKVFGVFSAK	326			Indels 0;	Gaps 0;
	RESULT 6						
Q48044		PRELIMINARY;		PRT;	631 AA.	Query Match	82.3%; Score 135;
AC	Q48044;					Best Local Similarity 83.9%;	DB 2; Length 630;
DT	01-NOV-1996	(TREMBLrel. 01, Created)				Matches 26;	Conservative 1; Mismatches 4;
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)				Indels 0;	Gaps 0;
DE	01-MAR-2004	(TREMBLrel. 26, Last annotation update)					
GN	Name=tbp2;						
OS	Haemophilus influenzae.						
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;						
OC	Pasteurellaceae; Haemophilus.						
OX	NCBI_TaxID=727;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=SB12;						
RX	MEDLINE=98228706; PubMed=8830248;						
RA	Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,						
RA	Harkness R.B., Pele S.C., Klein M.H.;						
RT	"Cloning and expression of the Haemophilus influenzae transferrin receptor genes";						
RT	receptor genes";						
RL	Mol. Microbiol. 19:575-586 (1996).						
DR	EMBL: U15055; AAC43931.1; -.						
DR	PIR: S70909; S70909.						
DR	GO: 0016020; C:membrane; IEA.						
DR	InterPro; IPR01677; Transferrin_bind.						
DR	Pfam: PF01298; Lipoprotein_5;						
SQ	SEQUENCE 630 AA;	69700 MW;	6PCB2D1B6B642C84	CRC64;		Query Match	82.3%; Score 135;
						Best Local Similarity 83.9%;	DB 2; Length 630;
Qy	1	LEGGFYGPKGPELGFPLAGDKKVFGVFSAK	31			Matches 26;	Conservative 1; Mismatches 4;
Db	296	LEGGFYGPNGBGLGKPLAGDKKVFGVFSAK	326			Indels 0;	Gaps 0;
	RESULT 7						
Q48045		PRELIMINARY;		PRT;	631 AA.	Query Match	82.3%; Score 135;
AC	Q48045;					Best Local Similarity 83.9%;	DB 2; Length 630;
DT	01-NOV-1996	(TREMBLrel. 01, Created)				Matches 26;	Conservative 1; Mismatches 4;
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)				Indels 0;	Gaps 0;
DE	01-MAR-2004	(TREMBLrel. 26, Last annotation update)					
GN	Name=tbp2;						
OS	Haemophilus influenzae.						
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;						
OC	Pasteurellaceae; Haemophilus.						
OX	NCBI_TaxID=727;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=SB12;						
RX	MEDLINE=98228706; PubMed=8830248;						
RA	Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,						
RA	Harkness R.B., Pele S.C., Klein M.H.;						
RT	"Cloning and expression of the Haemophilus influenzae transferrin receptor genes";						
RT	receptor genes";						
RL	Mol. Microbiol. 19:575-586 (1996).						
DR	EMBL: U15055; AAC43931.1; -.						
DR	PIR: S70909; S70909.						
DR	GO: 0016020; C:membrane; IEA.						
DR	InterPro; IPR01677; Transferrin_bind.						
DR	Pfam: PF01298; Lipoprotein_5;						
SQ	SEQUENCE 630 AA;	69700 MW;	6PCB2D1B6B642C84	CRC64;		Query Match	82.3%; Score 135;
						Best Local Similarity 83.9%;	DB 2; Length 630;
Qy	1	LEGGFYGPKGPELGFPLAGDKKVFGVFSAK	31			Matches 26;	Conservative 1; Mismatches 4;
Db	296	LEGGFYGPNGBGLGKPLAGDKKVFGVFSAK	326			Indels 0;	Gaps 0;

RA Harkness R.E.; Pele S.c.; Klein M.H.; "Cloning and expression of the Haemophilus influenzae transferrin receptor genes." Mol. Microbiol. 19:575-586 (1996).

RT "Cloning and expression of the Haemophilus influenzae transferrin receptor genes." Pele S.c.; Klein M.H.; Harkness R.E.; Mol. Microbiol. 19:575-586 (1996).

RL PIR; S70910; AAC43333.1; -.

DR GO; GO:004998; P:transferrin receptor activity; IEA.

DR InterPro; IPR001677; Transferrin_bind.

DR PF01298; Lipoprotein 5; 1.

DR SEQNCB 631 AA; 70104 MW; E43FF90516F4EDC9 CRC64;

Query Match 82.3%; Score 135; DB 2; Length 631; Best Local Similarity 83.9%; Pred. No. 6e-10; Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGGYGPKGEBLGPFLAGDKKVPGVFSAK 31

Db 296 LEGGGYGPNAEBLGGFLANDBKVKPGVFSAK 326

RESULT 6

Q48034 PRELIMINARY; PRT; 644 AA.

AC DT 01-NOV-1996 (T-EMBLrel. 01, Created) DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)

DB Transferrin binding protein 2.

GN Name=tbpB;

OS Haemophilus influenzae.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus.

OC NCBI_TaxID=727;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=DLC63;

RX MEDLINE=95197237; PubMed=7890373;

RA Gray-Owen S.D.; Loosmore S.; Schryvers A.B.; "Identification and characterization of genes encoding the human transferrin-binding proteins from Haemophilus influenzae." Infect. Immun. 63:1201-1210 (1995).

RL GO; GO:0016020; C:membrane; IEA.

DR InterPro; IPR001677; Transferrin_bind.

DR PF01298; Lipoprotein 5; 1.

DR SEQNCB 644 AA; 70797 MW; 61399627DB422616 CRC64;

Query Match 79.9%; Score 131; DB 2; Length 644; Best Local Similarity 80.6%; Pred. No. 2.2e-09; Matches 25; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LEGGGYGPKGEBLGPFLAGDKKVPGVFSAK 31

Db 294 LEGGGYGPQGDELGGFLANDBKVKPGVFSAK 324

RESULT 7

Q48038 PRELIMINARY; PRT; 654 AA.

AC DT 01-NOV-1996 (T-EMBLrel. 01, Created) DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)

DB Transferrin binding protein 2.

GN Name=tbp2;

OS Haemophilus influenzae.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus.

OC NCBI_TaxID=727;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=PAK 12085; PubMed=8830248; RX MEDLINE=95228706; PubMed=8830248; RA Loosmore S.M.; Yang Y.P.; Coleman D.C.; Shortreed J.M.; England D.M., "Cloning and expression of the Haemophilus influenzae transferrin receptor genes." Pele S.c.; Klein M.H.; Harkness R.E.; Mol. Microbiol. 19:575-586 (1996).

RT "Cloning and expression of the Haemophilus influenzae transferrin receptor genes." Mol. Microbiol. 19:575-586 (1996).

RL PIR; S70905; S70905.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:004998; P:transferrin receptor activity; IEA.

DR InterPro; IPR001677; Transferrin_bind.

DR PF01298; Lipoprotein 5; 1.

DR SEQNCB 654 AA; 71834 MW; PPJEC728BE5F05A6 CRC64;

Query Match 79.9%; Score 131; DB 2; Length 654; Best Local Similarity 80.6%; Pred. No. 2.2e-09; Matches 25; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGGYGPKGEBLGPFLAGDKKVPGVFSAK 31

Db 296 LEGGGYGPNAEBLGGFLANDBKVKPGVFSAK 326

RESULT 8

Q6H804 PRELIMINARY; PRT; 566 AA.

AC Q6H804; PRELIMINARY; PRT; 566 AA.

DR 05-JUL-2004 (TREMBLrel. 27, Created)

DR 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DR 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DB Transferrin binding protein B (Fragment). GN Name=tbpB;

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.

OC NCBI_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Alpha26;

RX Harrison O.B.; Claus H.; Vogel U.; Bennett J.; Maiden M.; Rokbi B.; Submitted (MAY 2004) to the EMBL/GenBank/DBPdb databases.

RL DR GO; GO:0016020; C:membrane; IEA.

DR DR InterPro; IPR001677; Transferrin_bind.

DR PF01298; Lipoprotein 5; 1.

FT NON-TBR 566 566 566 AA; 61751 MW; B0PC99B682412D8 CRC64;

FT SEQNCB 566 AA; 61751 MW; B0PC99B682412D8 CRC64;

Query Match 77.4%; Score 127; DB 2; Length 566; Best Local Similarity 77.4%; Pred. No. 6.8e-09; Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGGYGPKGEBLGPFLAGDKKVPGVFSAK 31

Db 291 LEGGGYGPQGDELGGFLANDBKVKPGVFSAK 321

RESULT 9

Q9FC53 PRELIMINARY; PRT; 582 AA.

AC Q9FC53; PRELIMINARY; PRT; 582 AA.

DR 01-MAR-2001 (TREMBLrel. 16, Created)

DR 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DR 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DB Transferrin binding protein B (Fragment). GN Name=tbpB;

OS Neisseria meningitidis (Bergroup B).

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.

OC NCBI_TaxID=491;

OX NCBI_TaxID=491;

[1]

RN [1]
SEQUENCE FROM N.A.
STRAIN=27/7;
RX MEDLINE=2407297; PubMed=1094100;
RX DOI=10.1128/IAI.68.4.938-4.947.2000;
RA Rokbi B.; Renaud-Mongenie G.; Mignon M.; Danve B.; Poncet D.;
RA Chabane C.; Caugant D.A.; Quentin-Millet M.J.;
RT "Allelic diversity of the two transferrin binding protein B genes
isotypes among a collection of *Neisseria meningitidis* strains
representative of serogroup B disease: implication for the composition
of a recombinant B vaccine.";
RL Infect. Immun. 68:938-947 (2000).
DR EMBL; AY279554; CAC05588.1;
GO; GO:0004998; F:transferrin receptor activity; IEA.
DR PF01298; C:membrane;
DR InterPro; IPR001677; Transferrin_bind.
Pfam; PF01298; Lipoprotein_5.1.
DR NON_TER 1 1
FT CHAIN <1 582
SEQUENCE 582 AA; 63426 MW; 2694AD04F2507F4 CRC64;
Query Match 77.4%; Score 127; DB 2; Length 592;
Best Local Similarity 77.4%; Pred. No. 7e-09;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 LEGGYGPKGKEBELGPRFLADDKVYFGVFSAK 31
Db 307 LEGGYGPKGKEBELGPRFLADDKVYFGVFSAK 337

RESULT 10
ID Q6HW3
ID Q6HW5 PRELIMINARY; PRT; 593 AA.
AC Q6HW5;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Transferrin binding protein B.
GN Name=tbpB;
OS *Neisseria cinerea*.
OC Bacteria; Proteobacteria; Betaproteobacteria; *Neisseriales*;
OC *Neisseriaceae*; *Neisseria*.
NCBI_TaxID=483;
RN [1]
RP SEQUENCE FROM N.A.
STRAIN=27/7;
RA Harrison O.B.; Claus H.; Vogel U.; Bennett J.; Maiden M.; Rokbi B.;
RT Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
EMBL; AY04731; CAG28813.2;
GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001677; Transferrin_bind.
Pfam; PF01298; Lipoprotein_5.1.
SEQUENCE 593 AA; 642.8 MW; 8F67EA15A9PEA9 CRC64;
Query Match 77.4%; Score 127; DB 2; Length 592;
Best Local Similarity 77.4%; Pred. No. 7.e-09;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 LEGGYGPKGKEBELGPRFLADDKVYFGVFSAK 31
Db 318 LEGGYGPKGKEBELGPRFLADDKVYFGVFSAK 348

RESULT 11
ID Q6HW6
ID Q6HW6 PRELIMINARY; PRT; 593 AA.
AC Q6HW6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Transferrin binding protein B.
GN Name=tbpB;

OS *Neisseria meningitidis*.
OC Bacteria; Proteobacteria; Betaproteobacteria; *Neisseriales*;
OC *Neisseriaceae*; *Neisseria*.
NCBI_TaxID=483;
RN [1]

[2]

RN [1]
SEQUENCE FROM N.A.
STRAIN=27/7;
RX MEDLINE=2407297; PubMed=1094100;
RX DOI=10.1128/IAI.68.4.938-4.947.2000;
RA Rokbi B.; Renaud-Mongenie G.; Mignon M.; Danve B.; Poncet D.;
RA Chabane C.; Caugant D.A.; Quentin-Millet M.J.;
RT "Allelic diversity of the two transferrin binding protein B genes
isotypes among a collection of *Neisseria meningitidis* strains
representative of serogroup B disease: implication for the composition
of a recombinant B vaccine.";
RL Infect. Immun. 68:938-947 (2000).
DR EMBL; AY279554; CAC05588.1;
GO; GO:0004998; F:transferrin receptor activity; IEA.
DR PF01298; C:membrane;
DR InterPro; IPR001677; Transferrin_bind.
Pfam; PF01298; Lipoprotein_5.1.
DR NON_TER 1 1
FT CHAIN <1 582
SEQUENCE 582 AA; 64257 MW; 45187C48497275BA CRC64;
Query Match 77.4%; Score 127; DB 2; Length 593;
Best Local Similarity 77.4%; Pred. No. 7.1e-09;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 LEGGYGPKGKEBELGPRFLADDKVYFGVFSAK 31
Db 318 LEGGYGPKGKEBELGPRFLADDKVYFGVFSAK 348

RESULT 12
ID Q6HW3
ID Q6HW3 PRELIMINARY; PRT; 594 AA.
AC Q6HW3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DB Transferrin binding protein B.
GN Name=tbpB;
OS *Neisseria flavescens*.
OC Bacteria; Proteobacteria; Betaproteobacteria; *Neisseriales*;
OC *Neisseriaceae*; *Neisseria*.
NCBI_TaxID=483;
RN [1]
RP SEQUENCE FROM N.A.
RC Harrison O.B.; Claus H.; Vogel U.; Bennett J.; Maiden M.; Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
EMBL; AY04731; CAG28813.2;
GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001677; Transferrin_bind.
Pfam; PF01298; Lipoprotein_5.1.
SEQUENCE 594 AA; 63190 MW; F096DB9E9B046D0B CRC64;
Query Match 77.4%; Score 127; DB 2; Length 594;
Best Local Similarity 77.4%; Pred. No. 7.1e-09;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 LEGGYGPKGKEBELGPRFLADDKVYFGVFSAK 31
Db 318 LEGGYGPKGKEBELGPRFLADDKVYFGVFSAK 348

RESULT 13
ID Q5391
ID Q5391 PRELIMINARY; PRT; 602 AA.
AC Q5391;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DB TbpB precursor.
GN Name=tbpB;

OS *Neisseria meningitidis*.
OC Bacteria; Proteobacteria; Betaproteobacteria; *Neisseriales*;
OC *Neisseriaceae*; *Neisseria*.
NCBI_TaxID=483;
RN [1]

RESULT 14

SEQUENCE FROM N.A.
STRAIN=2713;
RX MEDLINE=98148004; PubMed=9479046; DOI=10.1016/S0378-1119(97)00646-X;
RA Legrain M.; Robbi B.; Villevie D.; Jacobs E.;
RT "Characterization of genetic exchanges between various highly divergent tbpB5, having occurred in *Neisseria meningitidis*."
RT EMBL: AJ223044; CAA11047; 1;
DR GO: GO:0016020; C:membrane; IEA.
GO: GO:0004998; P:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
KW SIGNAL. 1 20 Potential.
PT CHAIN 21 602 TbpB.
SQ SEQUENCE 602 AA; 65488 MW; 74641BF77B61C257 CRC64;
Query Match 77.4%; Score 127; DB 2; Length 602;
Best Local Similarity 77.4%; Pred. No. 7.2e-09;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Db 327 LEGGPYGPKGEBLGPFLAGDKKVKVFGVFSAK 31
LEGGPYGPKGEBLGPFLAGDKKVKVFGVFSAK 357

RESULT 15

SEQUENCE FROM N.A.
STRAIN=414, and 3191;
RA Harrison O.B.; Claus H.; Vogel U.; Bennett J.; Maiden M.; Robbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
EMBL; AU704736; CAG8818.2;
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004998; P:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SEQUENCE 594 AA; 64345 MW; 6200B465E793F20A CRC64;
Query Match 76.2%; Score 125; DB 2; Length 594;
Best Local Similarity 77.4%; Pred. No. 1.3e-08;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Db 318 LEGGPYGPQGDBLGGKFLAKDKKVKLAVFSAK 348
LEGGPYGPQGDBLGGKFLAKDKKVKLAVFSAK 348

RESULT 16

SEQUENCE FROM N.A.
STRAIN=3656;
RA Harrison O.B.; Claus H.; Vogel U.; Bennett J.; Maiden M.; Robbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
EMBL; AU704735; CAG28817.2;
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004998; P:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SEQUENCE 594 AA; 64331 MW; 7663C043033D615B CRC64;
Query Match 76.2%; Score 125; DB 2; Length 594;
Best Local Similarity 77.4%; Pred. No. 1.3e-08;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Search completed: November 9, 2005, 19:16:34
Job time : 134.914 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 9, 2005, 19:01:45 ; Search time 25.642 Seconds
(without alignments)
116.322 Million cell updates/sec

Title: US-10-043-344-50
Perfect score: 164
Sequence: 1 LEGGFYGPKGRLGFRPLAGDKCKVFGVFSAK 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : Listing First 45 summaries

PIR 79:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	147	89.6	625	2	D64107		transferrin-bindin
2	145	88.4	648	2			transferrin-bindin
3	139	84.8	631	2	S70908		transferrin-bindin
4	135	82.3	630	2	S70909		transferrin-bindin
5	135	82.3	631	2	S70910		transferrin-bindin
6	131	79.9	654	2	S70905		transferrin-bindin
7	125	76.2	660	2	S70904		transferrin-bindin
8	119	72.6	711	2	S70660		transferrin-bindin
9	115	70.1	547	2	S49815		transferrin-bindin
10	115	70.1	547	2	A44796		transferrin-bindin
11	115	70.1	689	2	D81832		transferrin-bindin
12	115	70.1	698	2	D81798		transferrin-bindin
13	114	69.5	599	2	JN0818		transferrin-bindin
14	111	67.7	711	2			transferrin-bindin
15	111	67.7	712	2	E81196		transferrin-bindin
16	105	64.0	547	2	S49814		transferrin-bindin
17	104	63.4	737	2	HB1070		lactoferrin-bindin
18	104	63.4	741	2	D81798		lactoferrin-bindin
19	102	62.2	593	2	S27483		transferrin-bindin
20	102	62.2	593	2	B44796		transferrin-bindin
21	66	40.2	488	2	E81003		transferrin-bindin
22	66	40.2	497	2	C82025		probable periplasm
23	62	37.8	289	2	G64105		transferrin-bindin
24	59	36.0	585	2	A83020		probable carboxymoyl
25	57	34.8	742	2	A49341		isocitrate dehydrogenase
26	54	32.9	389	2	T44975		lmp
27	52	32.0	521	2	T27606		hypothetical prote
28	52	31.7	316	2	T19435		hypothetical prote
29	52	31.7	539	2	T28770		hypothetical prote

ALIGNMENTS

RESULT 1
D64107
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: D64107
R;Pleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.R.; Weidman, J.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.T.; Glodek, A.; Kelley, J.M.; Weidman, J.D.M.; Brandon, R.C.; Pine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.; Science 269, 496-512, 1995
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Accession: D64107
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Cross-references: UNIPROT:R44971; GB:U32780; GB:LI42023; NID:91574020; PMID:9535030; PMID:1542800
A;Cross-references: UNIPROT:R44971; GB:U32780; GB:LI42023; NID:91574020; PMID:9535030; PMID:1542800
A;Genetics:
A;Gene: tbp2
C;Superfamily: bacterial pathogen transferrin-binding protein
C;Domain: signal sequence #Bstatus predicted <SIG>
F;1-17/Domain: signal sequence #Bstatus predicted <SIG>
F;18-625/Product: transferrin-binding protein 2 #status predicted <MAT>
Query Match 89.6%; Score 147; DB 2; Length 625;
Best Local Similarity 90.3%; Pred. No. 1..1e-12;
Matches 28; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 LEGGFYGPKGRLGFRPLAGDKCKVFGVFSAK 31
Db 293 LEGGFYGPKGRLGFRPLAGDKCKVFGVFSAK 323
RESULT 2
S70907
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB12)
C;Species: Haemophilus influenzae
C;Variety: strain SB12
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S70907; S73320
R;Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Hartness, R.E.; Mol. Microbiol. 19, 575-586, 1995
A;Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes
A;Reference number: S70907
A;Accession: S70907
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q48040; EMBL:U15054
A;Experimental source: strain SB12, clone DS-1047-1-2
R;Loosmore, S.M.; submitted to the EMBL Data Library, September 1994

A; Reference number: S73320
 A; Accession: S73320
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-630 <LOO>
 A; Cross-references: EMBL:U15054; NID:gi1223946; PIDN: AAC43930.1; PMID:91223947
 A; Experimental source: strain SB12, clone DS-1047-1-2
 C; Genetics:
 A; Gene: Cbp2
 C; Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
 F; 1-17/Domain: signal sequence #status predicted <SIG>
 F; 18-648/Product: transferrin-binding protein 2 #status predicted <MAT>
 Query Match 88.4%; Score 145; DB 2; Length 648;
 Best Local Similarity 87.1%; Pred. No. 2.2e-12; Indels 0; Gaps 0;
 Matches 27; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 LEGGFYGPKGEBLGRFLAGDKKVFGVFSAK 31
 Db 297 LEGGFYGPGEBOGLGKFLAGDKKVFGVFSAK 327

RESULT 3
 S70908 transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB29)
 A; Species: Haemophilus influenzae
 A; Variety: strain SB29
 C; Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C; Accession: S70908; S73321
 R; Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E
 Mol; Microbiol. 19, 575-586, 1996
 A; Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes
 A; Reference number: S70901; PMID:96228706; PMID:8830348
 A; Accession: S70908
 A; Molecule type: DNA
 A; Residues: 1-631 <LOO>
 A; Cross-references: UNIPROT:Q48041; EMBL:U15055
 A; Experimental source: strain SB29, clone DS-1090-3-2
 R; Loosmore, S.M.
 Submitted to the EMBL Data Library, September 1994
 A; Reference number: S73320
 A; Accession: S73321
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-250, 'L', 252-349, 'RTDATTN', 357-631 <LOW>
 A; Cross-references: EMBL:U15055; NID:gi1223948; PIDN: AAC43331.1; PMID:91223949
 A; Experimental source: strain SB29, clone DS-1090-3-2
 C; Genetics:
 A; Gene: Cbp2
 C; Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
 F; 1-17/Domain: signal sequence #status predicted <SIG>
 F; 18-631/Product: transferrin-binding protein 2 #status predicted <MAT>
 Query Match 84.8%; Score 139; DB 2; Length 631;
 Best Local Similarity 83.9%; Pred. No. 1.5e-11; Indels 0; Gaps 0;
 Matches 26; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 4
 S70909 transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB30)
 A; Species: Haemophilus influenzae
 A; Variety: strain SB30
 C; Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C; Accession: S70909; S73322
 R; Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E
 Mol; Microbiol. 19, 575-586, 1996
 A; Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes
 A; Reference number: S70901; PMID:96228706; PMID:8830348

RESULT 5
 S70910 transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB32)
 C; Species: Haemophilus influenzae
 C; Variety: strain SB32
 C; Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C; Accession: S70910; S73323
 R; Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E
 Mol; Microbiol. 19, 575-586, 1996
 A; Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes
 A; Reference number: S70901; PMID:96228706; PMID:8830348
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-631 <LOO>
 A; Cross-references: UNIPROT:Q48043; EMBL:U15057
 A; Experimental source: strain SB32, clone DS-1047-4-10
 R; Loosmore, S.M.
 Submitted to the EMBL Data Library, September 1994
 A; Reference number: S73320
 A; Accession: S73323
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-241, 'P', 243-420, 'C', 422-508, 'A', 510-631 <LOW>
 A; Cross-references: EMBL:U15057; NID:gi1223952; PIDN: AAC43933.1; PMID:91223953
 A; Experimental source: strain SB32, clone DS-1047-4-10
 C; Genetics:
 A; Gene: Cbp2
 C; Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
 F; 1-17/Domain: signal sequence #status predicted <SIG>
 F; 18-631/Product: transferrin-binding protein 2 #status predicted <MAT>
 Query Match 82.3%; Score 135; DB 2; Length 631;
 Best Local Similarity 83.9%; Pred. No. 5.5e-11; Indels 0; Gaps 0;
 Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 LEGGFYGPKGEBLGRFLAGDKKVFGVFSAK 31
 Db 296 LEGGFYGPNGEBLGRFLAGDKNRYFGVFSAK 326

RESULT 6
 S70905

transferrin-binding protein 2 precursor - Haemophilus influenzae (strain PAK 12085)

C;Accession: S70660
R;Legrain, M.; Findeli, A.; Villeval, D.; Quentin-Millet, M.J.; Jacobs, E.
C;Species: Haemophilus influenzae
A;Variety: strain PAK 12085
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S70905
R;Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E
Mol. Microbiol. 19, 575-586, 1996
A;Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes
A;Reference number: S70901; MUID:96228706; PMID:8830248
A;Accession: PIDN:9177568; NID:9177568; PIDN:CAA90588.1; PID:9117
A;Status: preliminary; nucleic acid sequence not shown
A;Cross-references: UNIPROT:Q48038; EMBL:U15053; NID:91223943; PIDN: AAC43928.1; PID:9122
A;Experimental source: strain PAK 12085
C;Genetics:
A;Gene: tbp2
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
P;1-17/Domain: signal sequence #status predicted <SIG>
P;18-654/Product: transferrin-binding protein 2 #status predicted <MAT>
Query Match 79.9%; Score 131; DB 2; Length 654;
Best Local Similarity 80.6%; Pred. No. 2.1e-10;
Matches 25; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Db 296 LEGGFYGPKGEBLGRFLAGDKKVKVGFSAK 31
Db 296 LEGGFYGPNAEELGKRFLANDEKVKVGFSAK 326

RESULT 9
S49815
transferrin-binding protein - *Actinobacillus pleuropneumoniae*
C;Species: *Actinobacillus pleuropneumoniae*
C;Date: 05-Mar-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S49815
R;Bunka, S.; Potter, A.; Gerlach, G.
submitted to the EMBL Data Library, November 1994
A;Description: Cloning and sequencing of the transferrin-binding protein genes of *Actinobacillus pleuropneumoniae*
A;Reference number: S49814
A;Accession: S49815
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q44168; EMBL:Z46775; NID:9577528; PIDN:CAA86730.1; PID:95775
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
Query Match 70.1%; Score 115; DB 2; Length 547;
Best Local Similarity 67.7%; Pred. No. 3.1e-08;
Matches 21; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
Db 272 LEGGFYGPKGEBLGRFLAGDKKVKVGFSAK 31
Db 272 LEGGFYGPNAEELGKRFLANDEKVKVGFSAK 302

RESULT 10
A44796
transferrin-binding protein, tfba - *Actinobacillus pleuropneumoniae*
C;Species: *Actinobacillus pleuropneumoniae*
C;Accession: A44796; S27484
R;Gerlach, G.F.; Klashinsky, S.; Anderson, C.; Porter, A.A.; Willson, P.J.
Infect. Immun. 60, 3253-3261, 1992
A;Title: Characterization of two genes encoding distinct transferrin-binding proteins in
A;Reference number: A44796; PMID:1639494
A;Content: A44796, serotype 7
A;Accession: A44796
A;Status: Preliminary
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q44170; EMBL:M85275; NID:9141842; PIDN:AAA21929.1; PID:91418
A;Residues: 1-547 <GBR>
A;Note: sequence inconsistent with the nucleotide translation
A;Sequence extracted from NCBI backbone (NCBInI:109735, NCBIP:109736)
C;Genetics:
A;Gene: tba

transferrin-binding protein 2 precursor - *Neisseria meningitidis*

C;Accession: S70660
R;Legrain, M.; Findeli, A.; Villeval, D.; Quentin-Millet, M.J.; Jacobs, E.
C;Species: *Neisseria meningitidis*
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S70905
R;Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E
Mol. Microbiol. 19, 575-586, 1996
A;Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes
A;Reference number: S70901; MUID:96228706; PMID:8830248
A;Accession: PIDN:9177568; NID:9177568; PIDN:CAA90588.1; PID:9117
A;Status: preliminary; nucleic acid sequence not shown
A;Cross-references: UNIPROT:Q31284; EMBL:Z50371; PIDN: AAC43928.1; PID:9122
A;Experimental source: strain PAK 12085
C;Genetics:
A;Gene: tbp2
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
C;Keywords: membrane protein
C;Keywords: signal sequence #status predicted <SIG>
P;1-20/Domain: signal sequence #status predicted <SIG>
P;21-711/Product: transferrin-binding protein 2 #status predicted <MAT>
Query Match 72.6%; Score 119; DB 2; Length 711;
Best Local Similarity 77.4%; Pred. No. 1.1e-08;
Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Db 335 LSGGFPKGEBLGRFLSDDKVKVAVGSAK 365

RESULT 9
S49815
transferrin-binding protein - *Actinobacillus pleuropneumoniae*
C;Species: *Actinobacillus pleuropneumoniae*
C;Date: 05-Mar-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S49815
R;Bunka, S.; Potter, A.; Gerlach, G.
submitted to the EMBL Data Library, November 1994
A;Description: Cloning and sequencing of the transferrin-binding protein genes of *Actinobacillus pleuropneumoniae*
A;Reference number: S49814
A;Accession: S49815
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q44168; EMBL:Z46775; NID:9577528; PIDN:CAA86730.1; PID:95775
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
Query Match 70.1%; Score 115; DB 2; Length 547;
Best Local Similarity 67.7%; Pred. No. 3.1e-08;
Matches 21; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
Db 272 LEGGFYGPNAEELGKRFLANDEKVKVGFSAK 31
Db 272 LEGGFYGPNAEELGKRFLANDEKVKVGFSAK 302

RESULT 10
A44796
transferrin-binding protein, tfba - *Actinobacillus pleuropneumoniae*
C;Species: *Actinobacillus pleuropneumoniae*
C;Accession: A44796; S27484
R;Gerlach, G.F.; Klashinsky, S.; Anderson, C.; Porter, A.A.; Willson, P.J.
Infect. Immun. 60, 3253-3261, 1992
A;Title: Characterization of two genes encoding distinct transferrin-binding proteins in
A;Reference number: A44796; PMID:1639494
A;Content: A44796, serotype 7
A;Accession: A44796
A;Status: Preliminary
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q44170; EMBL:M85275; NID:9141842; PIDN:AAA21929.1; PID:91418
A;Residues: 1-547 <GBR>
A;Note: sequence inconsistent with the nucleotide translation
A;Sequence extracted from NCBI backbone (NCBInI:109735, NCBIP:109736)
C;Genetics:
A;Gene: tba

C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a

Query Match 70.1%: Score 115; DB 2; Length 547;
Best Local Similarity 67.7%; Pred. No. 3.1e-08;
Matches 21; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LEGGFYGPKGEBLGRPLAGDKKVKVGFVSAK 31
Db 272 LEGGFYGPKGEBLGRPLAGDKKVKVGFVSAK 302

RESULT 11

transferrin-binding protein 2 precursor - *Neisseria meningitidis*
C;Species: *Neisseria meningitidis*
C;Accession: S70661; S37626; S70659
R;Legrain, M.
submitted to the EMBL Data Library, August 1995
A;Reference number: S70661
A;Accession: S70661
A;Molecule type: DNA
A;Residues: 1-69 <LEG>
A;Cross-references: UNIPROT:Q51288; EMBL:250732; NID:91177570; PIDN:CAA90599.1; PID:9117
A;Experimental source: strain B283
R;Wilton, J.; Ala'Aldien, D.; Palmer, H.M.; Borriello, S.P.
FEMS Microbiol. Lett. 107, 59-66, 1993
A;Title: Cloning and partial sequence of transferrin-binding protein 2 of *Neisseria meningitidis*
A;Accession: S37626
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 25-65 <WIL>
A;Cross-references: EMBL:X75167; NID:9405780; PIDN:CAA53009.1; PID:9405781
R;Legrain, M.; Finsel, A.; Villeval, D.; Quentin-Millet, M.J.; Jacobs, R.
Mol. Microbiol. 19, 159-169, 1996
A;Title: Molecular characterization of hybrid Tbp2 proteins from *Neisseria meningitidis*.
A;Reference number: S70659; PMID:96419172; PMID:8821945
A;Accession: S70659
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 21-245, 'D', 247-260, 'D', 262-689 <LEW>
A;Cross-references: EMBL:250732
C;Genetics:

Query Match 70.1%: Score 115; DB 2; Length 689;
Best Local Similarity 74.2%; Pred. No. 3.9e-08;
Matches 23; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEGGFYGPKGEBLGRPLAGDKKVKVGFVSAK 31
Db 312 LEGGFYGPKGEBLGRPLAGDKKVKVGFVSAK 342

RESULT 12

transferrin-binding protein B NMA02025 [imported] - *Neisseria meningitidis* (strain Z2491)
C;Species: *Neisseria meningitidis*
C;Accession: D81832
C;Cross-references: D81832
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Hollroyd, S.; Jagels, K.; Leather, S.; Mungall, K.; Quail, M.A.; Rajandream, NATURE 40, 505-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A;Accession: D81832
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-698 <PAR>
A;Cross-references: UNIPROT:Q68937; GB:AL162757; GB:AL157959; NID:97380371; PIDN:CA8524
A;Experimental source: Serogroup A, strain Z2491
C;Genetics:
A;Gene: tbpB; NMA02025
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a

Query Match 70.1%: Score 115; DB 2; Length 698;
Best Local Similarity 74.2%; Pred. No. 3.9e-08;
Matches 23; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEGGFYGPKGEBLGRPLAGDKKVKVGFVSAK 31
Db 322 LEGGFYGPKGEBLGRPLAGDKKVKVGFVSAK 352

RESULT 13

transferrin-binding protein 2 precursor - *Neisseria meningitidis* (strain B16B6)
C;Species: *Neisseria meningitidis*
C;Accession: JN0818; PN0633; S33153
R;Legrain, M.; Marzin, V.; Irwin, S.W.; Bouchon, B.; Quentin-Millet, M.J.; Jacobs, E.; Gene 130, 73-80, 1993
A;Title: Cloning and characterization of *Neisseria meningitidis* genes encoding the trans
A;Reference number: JN0818; MUID:93345825; PMID:8344530
A;Accession: JN0818
A;Cross-references: UNIPROT:Q06988; EMBL:215129;
A;Molecule type: DNA
A;Residues: 1-599 <LEG>
A;Accession: PN0633
A;Molecule type: protein
A;Residues: 21-34;51-61;158-171;351-361;363-368;378-386;441-456;564-582 <LE1>
C;Genetics:
A;Gene: tbp2
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
C;Keywords: iron transport; membrane protein; metal binding
F;1-20/Domain: signal sequence #status predicted <SG>
F;21-599/Domain: transferrin-binding protein 2 #status predicted <MAT>
Query Match 69.5%: Score 114; DB 2; Length 599;
Best Local Similarity 71.0%; Pred. No. 4.6e-08;
Matches 22; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 LEGGFYGPKGEBLGRPLAGDKKVKVGFVSAK 31
Db 315 LEGGFYGPKGEBLGRPLAGDKKVKVGFVSAK 345

RESULT 14

transferrin-binding protein 2 precursor - *Neisseria meningitidis* (strain M982)
C;Species: *Neisseria meningitidis*
C;Accession: JN0820; PN0635; S33155
R;Legrain, M.; Marzin, V.; Irwin, S.W.; Bouchon, B.; Quentin-Millet, M.J.; Jacobs, E.; Gene 130, 73-80, 1993
A;Title: Cloning and characterization of *Neisseria meningitidis* genes encoding the trans
A;Reference number: JN0818; MUID:93345825; PMID:8344530
A;Accession: JN0820
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-711 <LEG>
A;Cross-references: D81832
A;Accession: PN0635
A;Molecule type: protein
A;Residues: 21-33;58-65;144-161;178-190;419-424 <LE1>
A;Gene: tbp2
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
C;Keywords: iron transport; membrane protein; metal binding

F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-71/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 67.7%; Score 111; DB 2; Length 711;
 Best Local Similarity 71.0%; Pred. No. 1.5e-07;
 Matches 22; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 LEGGFYCPKGBELGFRPLAGDKRKFVFGVFSAK 31
 Db 335 LSGGFPGPQGBELGFRPLSDDKVAVVGSAK 365

RESULT 15

E81196 transferrin-binding protein 2 NMB0460 [imported] - *Neisseria meningitidis* (strain MC58) 8
 C;Species: *Neisseria meningitidis*
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C;Accession: E81196
 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jefferies, A.C.; Nelson, K.B.; Eisen, J.A.
 Hickie, B.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
 Ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
 Science 287, 1809-1815, 2000
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; ve
 A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A;Reference number: A81000; MUID:2017575; PMID:1070307
 A;Accession: E81196
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-712 <PTM>
 A;Cross references: UNIPROT:Q9K0V0; GB:AE002402; GB:g7225683; PIDN:AAF4089
 A;Experimental source: serogroup B, strain MC58
 C;Genetics:
 A;Gene: NMB0460
 C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
 Query Match 67.7%; Score 111; DB 2; Length 712;
 Best Local Similarity 71.0%; Pred. No. 1.5e-07;
 Matches 22; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 LEGGFYCPKGBELGFRPLAGDKRKFVFGVFSAK 31
 Db 336 LSGGFPGPQGBELGFRPLSDDKVAVVGSAK 366

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 Job time : 26.642 secs

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Page 1

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GenCore version 5.1.6

protein - protein search, using sw model

on: November 9, 2005, 18:37:18 ; Search time 132.802 Seconds
(without alignments)

97.669 Million cell updates/sec

file: US-10-043-344-50

perfect score: 164

Sequence: 1 LEGGFYGPGBELGFRFLAGDKRVEGVPSAK 31

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searched: 1867879 seqs, 418409474 residues

total number of hits satisfying chosen parameters: 1867879

minimum DB seq length: 0

maximum DB seq length: 2000000000

1st-processing: Maximum Match 0%
Maximum Match 100%
Listing First 45 summaries

database :

Published Applications AA:
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RESULTS

RESULT 1

US-10-043-344-50

; Sequence 50, Application US/10043344
; Publication No. US20030088086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin B.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michael H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221.MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIORITY APPLICATION NUMBER: 08/649,518
; PRIORITY FILING DATE: 1996-05-17
; NUMBER OF SEQ ID Nos: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Haemophilus influenzae

SEQUENCES

1 LEGGFYGPGBELGFRFLAGDKRVEGVPSAK 31
1 LEGGFYGPGBELGFRFLAGDKRVEGVPSAK 31

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

Result No.	Score	Query Match Length	DB ID	Description
1	164	100.0	31	14 US-10-043-344-50
2	145	88.4	648	14 US-10-043-344-109
3	139	84.8	631	14 US-10-043-344-111
4	135	82.3	630	14 US-10-043-344-113
5	135	82.3	631	14 US-10-043-344-111
6	131	79.9	644	14 US-10-043-344-6
7	131	79.9	654	14 US-10-043-344-12
8	125	76.2	365	14 US-10-043-344-156
9	125	76.2	404	14 US-10-043-344-155
10	125	76.2	411	14 US-10-043-344-153
11	125	76.2	417	14 US-10-043-344-153

RESULT 2
 US-10-043-344-109
 ; Sequence 109, Application US/10043344
 ; Publication No. US20030088086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Loosmore, Sheena M.
 ; APPLICANT: Harkness, Robin E.
 ; APPLICANT: Schryvers, Anthony B.
 ; APPLICANT: Chong, Pele
 ; APPLICANT: Gray-Owen, Scott
 ; APPLICANT: Murdin, Andrew D.
 ; APPLICANT: Klein, Michel H.
 ; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
 ; FILE REFERENCE: 1038-1221 MIS
 ; CURRENT APPLICATION NUMBER: US/10/043,344
 ; CURRENT FILING DATE: 2002-07-01
 ; PRIORITY NUMBER: 08/649,518
 ; PRIORITY FILING DATE: 1996-05-17
 ; NUMBER OF SEQ ID NOS: 160
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 109
 ; LENGTH: 648
 ; TYPE: PRT
 ; ORGANISM: Haemophilus influenzae
 ; US-10-043-344-109
 Query Match 88.4%; Score 145; DB 14; Length 648;
 Best Local Similarity 87.1%; Pred. No. 1.1e-12;
 Matches 27; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 LEGGGYGPKEBELGPRFLAGDKKVFGVFSAK 31
 Db 297 LEGGGYGPKEBELGPRFLAGDKKVFGVFSAK 327
 RESULT 5
 US-10-043-344-115
 ; Sequence 115, Application US/10043344
 ; Publication No. US20030088086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Loosmore, Sheena M.
 ; APPLICANT: Harkness, Robin E.
 ; APPLICANT: Schryvers, Anthony B.
 ; APPLICANT: Chong, Pele
 ; APPLICANT: Gray-Owen, Scott
 ; APPLICANT: Murdin, Andrew D.
 ; APPLICANT: Klein, Michel H.
 ; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
 ; FILE REFERENCE: 1038-1221 MIS
 ; CURRENT APPLICATION NUMBER: US/10/043,344
 ; CURRENT FILING DATE: 2002-07-01
 ; PRIORITY NUMBER OF SEQ ID NOS: 160
 ; PRIORITY FILING DATE: 1996-05-17
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 115
 ; LENGTH: 631
 ; TYPE: PRT
 ; ORGANISM: Haemophilus influenzae
 ; US-10-043-344-115
 Query Match 82.3%; Score 135; DB 14; Length 630;
 Best Local Similarity 83.9%; Pred. No. 3.3e-11;
 Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 LEGGGYGPKEBELGPRFLAGDKKVFGVFSAK 31
 Db 296 LEGGGYGPKEBELGPRFLAGDKKVFGVFSAK 326
 RESULT 6
 US-10-043-344-6
 ; Sequence 6, Application US/10043344
 ; Publication No. US20030088086A1
 ; GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena M.
 APPLICANT: Harkness, Robin E.
 APPLICANT: Schryvers, Anthony B.
 APPLICANT: Chong, Pele
 APPLICANT: Gray-Owen, Scott
 APPLICANT: Murdin, Andrew D.
 APPLICANT: Klein, Michel H.
 TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
 FILE REFERENCE: 1038-1221 MIS
 CURRENT APPLICATION NUMBER: US/10/043,344
 CURRENT FILING DATE: 2002-07-01
 PRIOR APPLICATION NUMBER: 08/649,518
 PRIOR FILING DATE: 1996-05-17
 NUMBER OF SEQ ID NOS: 160
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 6
 LENGTH: 644
 TYPE: PRT
 ORGANISM: Haemophilus influenzae
 US-10-043-344-6

Query Match 79.9%; Score 131; DB 14; Length 644;
 Best Local Similarity 80.6%; Pred. No. 1.3e-10;
 Matches 25; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LEGGGFVGPKGEBELGPRFLAGDKKVGVFSAK 31
 Db 294 LEGGGFVGPKGEBELGPRFLAGDKKVGVFSAK 324

RESULT 7
 US-10-043-344-12
 Sequence 12, Application US/10043344
 Publication No. US20030088086A1
 GENERAL INFORMATION:
 APPLICANT: Loosmore, Sheena M.
 APPLICANT: Harkness, Robin E.
 APPLICANT: Schryvers, Anthony B.
 APPLICANT: Chong, Pele
 APPLICANT: Gray-Owen, Scott
 APPLICANT: Murdin, Andrew D.
 APPLICANT: Klein, Michel H.
 TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
 FILE REFERENCE: 1038-1221 MIS
 CURRENT APPLICATION NUMBER: US/10/043,344
 CURRENT FILING DATE: 2002-07-01
 PRIOR APPLICATION NUMBER: 08/649,518
 NUMBER OF SEQ ID NOS: 160
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 12
 LENGTH: 654
 TYPE: PRT
 ORGANISM: Haemophilus influenzae
 US-10-043-344-12

Query Match 79.9%; Score 131; DB 14; Length 654;
 Best Local Similarity 80.6%; Pred. No. 1.3e-10;
 Matches 25; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGGFVGPKGEBELGPRFLAGDKKVGVFSAK 31
 Db 296 LEGGGFVGPKGEBELGPRFLAGDKKVGVFSAK 326

RESULT 8
 US-10-043-344-156
 Sequence 156, Application US/10043344
 Publication No. US20030088086A1
 GENERAL INFORMATION:
 APPLICANT: Loosmore, Sheena M.
 APPLICANT: Harkness, Robin E.
 APPLICANT: Schryvers, Anthony B.
 APPLICANT: Chong, Pele
 APPLICANT: Gray-Owen, Scott
 APPLICANT: Murdin, Andrew D.
 APPLICANT: Klein, Michel H.
 TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
 FILE REFERENCE: 1038-1221 MIS
 CURRENT APPLICATION NUMBER: US/10/043,344
 CURRENT FILING DATE: 2002-07-01
 PRIOR APPLICATION NUMBER: 08/649,518
 NUMBER OF SEQ ID NOS: 160
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 156
 LENGTH: 365
 TYPE: PRT
 ORGANISM: Haemophilus influenzae
 US-10-043-344-156

Query Match 76.2%; Score 125; DB 14; Length 365;
 Best Local Similarity 77.4%; Pred. No. 5.5e-10;
 Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEGGGFVGPKGEBELGPRFLAGDKKVGVFSAK 31
 Db 294 LEGGGFVGPKGEBELGPRFLAGDKKVGVFSAK 324

RESULT 10
 US-10-043-344-154
 Sequence 154, Application US/10043344
 Publication No. US20030088086A1
 GENERAL INFORMATION:
 APPLICANT: Loosmore, Sheena M.
 APPLICANT: Harkness, Robin E.
 APPLICANT: Schryvers, Anthony B.
 APPLICANT: Chong, Pele
 APPLICANT: Gray-Owen, Scott
 APPLICANT: Murdin, Andrew D.
 APPLICANT: Klein, Michel H.
 TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
 FILE REFERENCE: 1038-1221 MIS
 CURRENT APPLICATION NUMBER: US/10/043,344
 CURRENT FILING DATE: 2002-07-01
 PRIOR APPLICATION NUMBER: 08/649,518
 NUMBER OF SEQ ID NOS: 160
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 155
 LENGTH: 404
 TYPE: PRT
 ORGANISM: Haemophilus influenzae
 US-10-043-344-155

Query Match 76.2%; Score 125; DB 14; Length 404;
 Best Local Similarity 77.4%; Pred. No. 6.2e-10;
 Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEGGGFVGPKGEBELGPRFLAGDKKVGVFSAK 31
 Db 294 LEGGGFVGPKGEBELGPRFLAGDKKVGVFSAK 324

APPLICANT: Klein, Michel H.
 TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
 FILE REFERENCE: 1038-1221 MIS
 CURRENT APPLICATION NUMBER: US/10/043,344
 CURRENT FILING DATE: 2002-07-01
 PRIOR APPLICATION NUMBER: 08/649,518
 PRIOR FILING DATE: 1996-05-17
 NUMBER OF SEQ ID NOS: 160
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 154
 LENGTH: 411
 TYPE: PRT
 ORGANISM: *Haemophilus influenzae*
 US-10-043-344-50

Query Match 76.2%; Score 125; DB 14; Length 411;
 Best Local Similarity 77.4%; Pred. No. 6.3e-10;
 Matches 24; Conservative 2; Nismatches 5; Indels 0; Gaps 0;
 Qy 1 LEGGFYGPKEBELGRFLAGDKKVYGVFSAK 31
 Db 294 LEGGFYGPNAEELGGKFLATDNRVFGVFSAK 324

RESULT 11
 US-10-043-344-153
 Sequence 153, Application US/10043344
 Publication No. US20030088086A1
 GENERAL INFORMATION:
 APPLICANT: Loosmore, Sheena M.
 APPLICANT: Harkness, Robin E.
 APPLICANT: Schryvers, Anthony B.
 APPLICANT: Chong, Pele
 APPLICANT: Gray-Owen, Scott
 APPLICANT: Murdin, Andrew D.
 APPLICANT: Klein, Michel H.
 TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
 FILE REFERENCE: 1038-1221 MIS
 CURRENT APPLICATION NUMBER: US/10/043,344
 CURRENT FILING DATE: 2002-07-01
 PRIOR APPLICATION NUMBER: 08/649,518
 PRIOR FILING DATE: 1996-05-17
 NUMBER OF SEQ ID NOS: 160
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 153
 LENGTH: 417
 TYPE: PRT
 ORGANISM: *Haemophilus influenzae*
 US-10-043-344-153

Query Match 76.2%; Score 125; DB 14; Length 417;
 Best Local Similarity 77.4%; Pred. No. 6.4e-10;
 Matches 24; Conservative 2; Nismatches 5; Indels 0; Gaps 0;
 Qy 1 LEGGFYGPKEBELGRFLAGDKKVYGVFSAK 31
 Db 294 LEGGFYGPNAEELGGKFLATDNRVFGVFSAK 324

RESULT 12
 US-10-043-344-152
 Sequence 152, Application US/10043344
 Publication No. US20030088086A1
 GENERAL INFORMATION:
 APPLICANT: Loosmore, Sheena M.
 APPLICANT: Harkness, Robin E.
 APPLICANT: Schryvers, Anthony B.
 APPLICANT: Chong, Pele
 APPLICANT: Gray-Owen, Scott
 APPLICANT: Murdin, Andrew D.
 APPLICANT: Klein, Michel H.
 TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
 FILE REFERENCE: 1038-1221 MIS
 CURRENT APPLICATION NUMBER: US/10/043,344
 CURRENT FILING DATE: 2002-07-01
 PRIOR APPLICATION NUMBER: 08/649,518

PRIOR FILING DATE: 1996-05-17
 NUMBER OF SEQ ID NOS: 160
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 150
 LENGTH: 529
 TYPE: PRT
 ORGANISM: Haemophilus influenzae
 US-10-043-344-150

Query Match 76.2%; Score 125; DB 14; Length 529;
 Best Local Similarity 77.4%; Pred. No. 8.3e-10;
 Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 LEGGFPYGPKGEBLGPFLAGDKKVFGVFSAK 31
 Db 294 LEGGFPYGPNAEELGGFLATDNRVFGVFSAK 324

RESULT 15
 US-10-043-344-149
 Sequence 149, Application US/10043344
 Publication No. US2003088086A1
 GENERAL INFORMATION:
 APPLICANT: Loosmore, Sheena M.
 APPLICANT: Harkness, Robin E.
 APPLICANT: Schryvers, Anthony B.
 APPLICANT: Chong, Peile
 APPLICANT: Gray-Owen, Scott
 APPLICANT: Murdin, Andrew D.
 APPLICANT: Klein, Michael H.
 TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
 FILE REFERENCE: 1038-1221 MIS
 CURRENT APPLICATION NUMBER: US/10/043,344
 CURRENT FILING DATE: 2002-07-01
 PRIOR APPLICATION NUMBER: 08/649,518
 PRIOR FILING DATE: 1996-05-17
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 149
 LENGTH: 547
 TYPE: PRT
 ORGANISM: Haemophilus influenzae
 US-10-043-344-149

Query Match 76.2%; Score 125; DB 14; Length 547;
 Best Local Similarity 77.4%; Pred. No. 8.6e-10;
 Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 LEGGFPYGPKGEBLGPFLAGDKKVFGVFSAK 31
 Db 294 LEGGFPYGPNAEELGGFLATDNRVFGVFSAK 324

Search completed: November 9, 2005, 19:10:50
 Job time : 133.802 secs

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Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	Alignments		
Searched:	1612378 seqs, 512079187 residues				
Total number of hits satisfying chosen parameters:	1612378				
Minimum DB seq length:	0				
Maximum DB seq length:	200000000				
Post-processing:	Minimum Match 0% Maximum Match 100%				
Database :	UniProt_03: 1: uniprot_sprot: 2: uniprot_trembl:				
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
	SUMMARIES				
Result No.	Query Score	Match Length	DB ID	Description	
1	186	100.0	644	2 Q48034	Q48034 haemophilus
2	172	92.5	648	2 Q48040	Q48040 haemophilus
3	159	85.5	625	1 TBP2_HARIN	P44971 haemophilus
4	159	85.5	630	2 Q48042	Q48042 haemophilus
5	159	85.5	631	2 Q48043	Q48043 haemophilus
6	157	84.4	654	2 Q48038	Q48038 haemophilus
7	156	83.9	631	2 Q48041	Q48041 haemophilus
8	150	80.6	660	2 Q57443	Q57443 haemophilus
9	136.5	73.4	566	2 Q6HB04	Q6HB04 neisseria m
10	136.5	73.4	582	2 Q9FC83	Q9FC83 neisseria m
11	136.5	73.4	593	2 Q6HB8W5	Q6HB8W5 neisseria s
12	136.5	73.4	593	2 Q6HB8W6	Q6HB8W6 neisseria s
13	136.5	73.4	594	2 Q6HB8W3	Q6HB8W3 neisseria f
14	136.5	73.4	602	2 Q53991	Q53991 neisseria m
15	134.5	72.3	594	2 Q6HB8W0	Q6HB8W0 neisseria f
16	134.5	72.3	594	2 Q6HB8W1	Q6HB8W1 neisseria f
17	132.5	71.2	593	2 Q6HB8V1	Q6HB8V1 neisseria s
18	132.5	71.2	593	2 Q6HB8W4	Q6HB8W4 neisseria f
19	132.5	71.2	594	2 Q6HB8V8	Q6HB8V8 neisseria m
20	124	66.7	713	2 Q85051	Q85051 moraxella c
21	121	65.1	702	2 Q85050	Q85050 moraxella c
22	118	63.4	711	2 Q9FD4	Q9FD4 moraxella c
23	118	63.4	712	2 Q92FD4	Q92FD4 moraxella c
24	118	63.4	714	2 Q85056	Q85056 moraxella c
25	115	61.8	706	2 Q85052	Q85052 moraxella c
26	115	61.8	709	2 Q85055	Q85055 moraxella c
27	114.5	61.6	571	2 Q6HB01	Q6HB01 neisseria m
28	113.5	61.0	410	2 Q6HB03	Q6HB03 neisseria m
29	113.5	61.0	567	2 Q6HB00	Q6HB00 neisseria m
30	113.5	61.0	569	2 Q6HB79	Q6HB79 neisseria m
	113.5	61.0	569	2 Q6HB02	Q6HB02 neisseria p

Run on:	November 9, 2005, 18:42:14 ; Search time 142.16 Seconds (without alignments) 126.074 Million cell updates/sec	Alignments
Title:	US-10-043-344-61	
Perfect score:	1 FRTSEGTLEGGFVGPQEGKPLAHDKKVLGVFS 35	
Sequence:		
Scoring table:	BLOSUM62	
Gapop 10.0 , Gapext 0.5		
SEARCHED		
RESULT 1		
Q48034	PRELIMINARY;	PRT; 644 AA.
ID Q48034;	AC Q48034;	PRELIMINARY;
AC Q48034;	ID Q48034;	PRELIMINARY;
DT 01-NOV-1996 (TREMBLrel. 01, Created)	DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	
DR Transferin binding protein 2.	DR Transferin binding protein 2.	
GN Name=tbpB;	GN Name=tbpB;	
OS Haemophilus influenzae.	OS Haemophilus influenzae.	
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales.	
OX NCBI_TaxID=727;	OX NCBI_TaxID=727;	
RN [1]	RN [1]	
SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	
STRAIN=D163;	STRAIN=D163;	
RX MEDLINE=95197237; PubMed=7890373;	RX MEDLINE=95197237; PubMed=7890373;	
RA Gray-Owen S.D., Loomore S., Schryvers A.B.;	RA Gray-Owen S.D., Loomore S., Schryvers A.B.;	
RT "Identification and characterization of genes encoding the human transferin-binding proteins from Haemophilus influenzae.";	RT "Identification and characterization of genes encoding the human transferin-binding proteins from Haemophilus influenzae.";	
RR transferin. Immun. 63:1201-1210(1995).	RR transferin. Immun. 63:1201-1210(1995).	
RL EMBL; U10882; AAA80491.1;	RL EMBL; U10882; AAA80491.1;	
DR GO; GO:0016020; C:membrane; IEA.	DR GO; GO:0016020; C:membrane; IEA.	
DR GO:004998; F:transferrin receptor activity; IEA.	DR GO:004998; F:transferrin receptor activity; IEA.	
DR InterPro; IPR001677; Transferrin_bind.	DR InterPro; IPR001677; Transferrin_bind.	
DR Pfam; PF01298; Lipoprotein_5_1.	DR Pfam; PF01298; Lipoprotein_5_1.	
SQ SEQUENCE 644 AA; 7079 MW; 610P9627D8422616 CRC64;	SQ SEQUENCE 644 AA; 7079 MW; 610P9627D8422616 CRC64;	
Query Match 100.0%; Score 186; DB 2; Length 644;	Query Match 100.0%; Score 186; DB 2; Length 644;	
Best Local Similarity 100.0%; Pred. NO. 1.2e-16;	Best Local Similarity 100.0%; Pred. NO. 1.2e-16;	
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 1 FTSEGTLLEGFVGPQEGKPLAHDKKVLGVFS 35	Qy 1 FTSEGTLLEGFVGPQEGKPLAHDKKVLGVFS 35	
Db 288 FTSEGTLLEGFVGPQEGKPLAHDKKVLGVFS 322	Db 288 FTSEGTLLEGFVGPQEGKPLAHDKKVLGVFS 322	
RESULT 2		
Q48040	PRELIMINARY;	PRT; 648 AA.
ID Q48040;	AC Q48040;	PRELIMINARY;
AC Q48040;	ID Q48040;	PRELIMINARY;
DT 01-NOV-1996 (TREMBLrel. 01, Created)	DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	
DR Transferin binding protein 2.	DR Transferin binding protein 2.	
GN Name=tbpB;	GN Name=tbpB;	
OS Haemophilus influenzae.	OS Haemophilus influenzae.	
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales.	
OX NCBI_TaxID=727;	OX NCBI_TaxID=727;	
RN [1]	RN [1]	
SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	
STRAIN=SB12;	STRAIN=SB12;	
RX MEDLINE=96228706; PubMed=8830248;	RX MEDLINE=96228706; PubMed=8830248;	

RA	Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M., Harkness R.B., Pele S.C., Klein M.H., "Cloning and expression of the Haemophilus influenzae transferrin receptor genes.", Mol. Microbiol. 19:575-586 (1996).	FT	CHAIN	18	625	Probable transferrin-binding protein 2.
RT	"Cloning and expression of the Haemophilus influenzae transferrin receptor genes.",	FT	LIPID	18	18	N-Palmitoyl cysteine (Probable).
RT	"Cloning and expression of the Haemophilus influenzae transferrin receptor activity.",	FT	LIPID	18	18	S-diacylglycerol Cysteine (Probable).
RL	EMBL: U105054; AAC4930.1; -.	SQ	SEQUENCE	625 AA;	69031 MW;	52EFBC77B5ED4B9A CRC64;
DR	PIR: S70907; S70907.	Query	Match	85.5%;	Score 159;	DB 1; Length 625;
DR	GO: 001620; C:membrane; IEA.	Best Local Similarity	85.7%;	Pred. No. 5.6e-13;		
DR	InterPro: IPR001677; Transferrin_bind.	Matches	30;	Conservative	1; Mismatches 4;	Indels 0;
DR	Pfam: PF01298; Lipoprotein_5.	Qy	1	FTSEGTLLEGFFYGPQEGLGGKFLAHDKVKGVS	35	Gaps 0;
SQ	SEQUENCE 648 AA; 71246 MW; D89690AE33891A5A CRC64;	Db	287	FTSEGTLLEGFFYGPQEGLGGKFLAHDKVKGVS	321	
RESULT 4						
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Q48042	PRELIMINARY;	PRT;	630 AA.		
Qy	1	FTSEGTLLEGFFYGPQEGLGGKFLAHDKVKGVS	35	ID	Q48042;	
Db	291	FTSEGTLLEGFFYGPQEGLGGKFLAHDKVKGVS	325	AC	Q48042;	
RESULT 3						
TBP2_HAEIN	STANDARD;	PRT;	625 AA.	ID	Q48042;	
ID	TBP2_HAEIN	STANDARD;	PRT;	AC	Q48042;	
AC	P44371;			DT	01-NOV-1995 (Rel. 32, Created)	
DT	01-NOV-1995 (Rel. 32, Last sequence update)	RP		DT	01-NOV-1996 (TREMBLrel. 01, Created)	
DT	25-OCT-2004 (Rel. 45, Last annotation update)	SEQUENCE FROM N.A.		DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
DE	Probable transferrin-binding protein 2 precursor.	RC		DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)	
GN	Name=tbp2; Synonyms=tbp2; OrderedlocusNames=HI0995;	MEDLINE=96228706; PubMed=8830248;		DB	Transferrin binding protein 2.	
OS	Haemophilus influenzae.	Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,		GN	Name=tbp2;	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;	Harkness R.E., Pele S.C., Klein M.H.,		OS	Haemophilus influenzae.	
OC	Pasteurellaceae; Haemophilus.	"Cloning and expression of the Haemophilus influenzae transferrin receptor genes.",		OC	Bacteria; Proteobacteria; Haemophilus; Pasteurellales;	
NCBI_TaxID=727;	RN	RT		NCBI_TaxID=727;	NCBI_TaxID=727;	
RN		RL				
RP	SEQUENCE FROM N.A.	DR				
RC	STRAIN=RD / KW20 / ATCC 51907;	PIR;				
RX	MEDLINE=95350630; PubMed=7512800;	GO; GO:0016020; C:membrane; IEA.				
RA	Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-P., Dougherty B.A., Merrick J.M., McKenney K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodck A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Heidelberg B., Cottam M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Sauder D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;	GO; GO:0004998; P:transferrin receptor activity; IEA.				
RA	"Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.",	InterPro: IPR001677; Transferrin_bind.				
RA	Science 269:496-512(1995).	DR				
CC	-I - FUNCTION: Acts as a transferrin receptor and is required for transferrin utilization (By similarity).	DR				
CC	-I - SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor (Probable).	DR				
CC	-----					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	DR				
CC	EMBL: U322780; AAC22657.1; -.	DR				
CC	PIR; D64107; D64107.	DR				
CC	InterPro: IPR001677; Transferrin_bind.	DR				
CC	Pfam: PF01298; Lipoprotein_5.	DR				
CC	PROKAR_LIPOPROTEIN_1.	DR				
CC	Complete proteome: Lipoprotein; Outer membrane; Palmitate; Receptor; Signal.	DR				
CC	1 17 Potential.	DR				

RT	receptor genes.";
RL	Mol. Microbiol. 19:575-586 (1996).
DR	EMBL; U15057; AAC43933.1; -.
PIR	S70101; S70910.
DR	GO:0016020; C:membrane; IEA.
DR	GO:0004998; P:transferrin receptor activity; IEA.
DR	InterPro; IPR001677; Transferrin_bind.
DR	Pfam; PF01298; Lipoprotein_5.1.
SQ	SEQUENCE 631 AA; 70104 MW; B43FF90516F4EDC9 CRC64;
Query Match	85.5%; Score 159; DB 2; Length 631;
Best Local Similarity	85.7%; Pred. No. 5.6e-13;
Matches	39; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Db	290 FTSEGTLEGFFYGPSEQELGGKFLAHDKTKVLGVFS 35
Qy	1 FTSEGTLEGFFYGPSEQELGGKFLAHDKTKVLGVFS 35
Db	290 FTSEGTLEGFFYGPNAEELGGKFLAHDKTKVLGVFS 324
RESULT 6	
Q48038	PRELIMINARY;
ID	Q48038
AC	Q48038; 01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DB	Transferrin binding protein 2.
GN	Name=tbpA;
OS	Haemophilus influenzae.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus.
OC	Pasteurellaceae; Haemophilus.
NCBI_TaxID	727;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=PAK 12085;
RX	MEDLINE=96228706; PubMed=8830248;
RA	Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M., Harkness R.E., Pele S.C., Klein M.H.;
RA	"Cloning and expression of the Haemophilus influenzae transferrin receptor genes.";
RT	Mol. Microbiol. 19:575-586 (1996).
RL	EMBL; U15057; AAC43928.1; -.
DR	PIR; S70055; S70905.
DR	GO:0016020; C:membrane; IEA.
DR	GO:0004998; P:transferrin receptor activity; IEA.
DR	InterPro; IPR001677; Transferrin_bind.
DR	Pfam; PF01298; Lipoprotein_5.1.
SQ	SEQUENCE 654 AA; 71834 MW; PP3EC720BESF05A6 CRC64;
Query Match	84.4%; Score 157; DB 2; Length 654;
Best Local Similarity	82.9%; Pred. No. 1.1e-12;
Matches	29; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Db	290 FTSEGTLEGFFYGPSEQELGGKFLAHDKTKVLGVFS 35
Qy	1 FTSEGTLEGFFYGPSEQELGGKFLAHDKTKVLGVFS 35
Db	290 FTSEGTLEGFFYGPNAEELGGKFLAHDKTKVLGVFS 324
RESULT 7	
Q48041	PRELIMINARY;
ID	Q48041
AC	Q48041; 01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DB	Transferrin binding protein 2.
GN	Name=tbpA;
OS	Haemophilus influenzae.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus.
OC	Pasteurellaceae; Haemophilus.
NCBI_TaxID	727;
RN	[1]
SEQUENCE FROM N.A.	
RC	Q6H804; PRELIMINARY;
AC	Q6H804; 05-JUL-2004 (TREMBLrel. 27, Created)
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DB	Transferrin binding protein B (Fragment).
GN	Name=tbpB;
Qy	1 FTSEGTLEGFFYGPSEQELGGKFLAHDKTKVLGVFS 35
Db	288 FTSEGTLEGFFYGPNAEELGGKFLAHDKTKVLGVFS 322
RESULT 9	
Q48041	PRELIMINARY;
ID	Q48041
AC	Q48041; 01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DB	Transferrin binding protein 2.
GN	Name=tbpA;
OS	Haemophilus influenzae.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus.
OC	Pasteurellaceae; Haemophilus.
NCBI_TaxID	727;
RN	[1]
SEQUENCE FROM N.A.	
RC	Q6H804; PRELIMINARY;
AC	Q6H804; 05-JUL-2004 (TREMBLrel. 27, Created)
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DB	Transferrin binding protein B (Fragment).
GN	Name=tbpB;

OS	Neisseria meningitidis.	AC	Q6H8W5;	DT	05-JUL-2004	(TREMBLrel.	27,	Created)
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;			DT	05-JUL-2004	(TREMBLrel.	27,	Last sequence update)
OC	Neisseriaceae; Neisseria.			DT	05-JUL-2004	(TREMBLrel.	27,	Last annotation update)
NCBI_TaxID=487;				DR	Transferrin binding protein B.			
RN	[1]			GN	Name=tbpB;			
RP	SEQUENCE FROM N.A.			OS	Neisseria cinerea.			
RC	STRAIN=Alpha261;			OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;			
RA	Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;			OC	Neisseriaceae; Neisseria.			
RL	Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.			NCBI_TaxID=483;				
DR	EMBL: AU074752; CG28834.1; -.			OX				
DR	GO: GO:0016020; C:membrane; IEA.			RN				
DR	InterPro: IPR001677; Transferrin receptor activity; IEA.			[1]	SEQUENCE FROM N.A.			
DR	PFAM: PF01298; Lipoprotein_5_1.			RC	STRAIN=415;			
FT	NON_TER 1 1			RA	Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;			
FT	NON_TER 566 566			RL	Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.			
SQ	SEQUENCE 566 AA; 61751 MW;			DR	EMBL: AU704731; CAG28813.2;			
	EOFCA9B682412D8 CRC64;			DR	GO: GO:0016020; C:membrane; IEA.			
Query Match	Best Local Similarity 73.4%; Score 136.5; DB 2; Length 566;			DR	GO: GO:0004998; F:transferrin receptor activity; IEA.			
Matches	Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;			DR	InterPro: IPR01677; Transferrin_bind.			
Db	1 FTSEG-TLEGGFYGPEGQBLGGKPLAHDKKVLYGFS 35			DR	PFAM: PF01298; Lipoprotein_5_1.			
	284 FVSDSDSLEGGFYGPQDGLGGKPLANDKKVLYAVS 319			SQ	SEQUENCE 593 AA; 64218 MW;			
RESULT 10				Query Match	73.4%; Score 136.5; DB 2; Length 593;			
Q9FC53	PRELIMINARY;	PRT;	582 AA.	Best Local Similarity	75.0%; Pred. No. 6.3e-10;			
ID	Q9FC53			Matches	27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;			
AC	Q9FC53;			Qy	1 FTSEG-TLEGGFYGPEGQBLGGKPLAHDKKVLYGFS 35			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			Db	311 FVSDSDSLEGGFYGPQDGLGGKPLANDKKVLYAVS 346			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)							
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)							
DB	Transferrin binding protein B (Fragment).							
GN	Name=tbpB;							
OS	Neisseria meningitidis (serogroup B).							
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;							
OC	Neisseriaceae; Neisseria.							
NCBI_TaxID=491;								
RN	[1]							
RP	SEQUENCE FROM N.A.							
RC	STRAIN=20407297; PubMed=10948108;							
RX	DOI=10.1182/STAI.6.9.1938-1947.2000;							
RX	RA							
RA	Rouaud Mongeon G., Mignon M., Danve B., Poncelet D.,							
RA	Chabaneil C., Caugant D.A., Quentin-Millet M.J.,							
RT	"Allelic diversity of the two transferrin binding protein B gene							
RT	isotypes among a collection of Neisseria meningitidis strains							
RT	representative of serogroup B disease: implication for the composition							
RT	of a recombinant TbpB-based vaccine.";							
RT	Infect. Immun. 68:4938-4947 (2000).							
DR	EMBL: AU279554; CPC05588.1; -.							
DR	GO: GO:0016020; C:membrane; IEA.							
DR	GO: GO:0004998; F:transferrin receptor activity; IEA.							
DR	InterPro: IPR001677; Transferrin_bind.							
DR	PFAM: PF01298; Lipoprotein_5_1.							
FT	NON_TER 1 1							
FT	CHAIN <1 582 AA; 63426 MW;							
FT	transferrin binding protein B.							
SQ	SEQUENCE 582 AA; 63426 MW;							
	26A94AD04F2507F4 CRC64;							
Query Match	Best Local Similarity 73.4%; Score 136.5; DB 2; Length 582;							
Matches	Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;							
Qy	1 FTSEG-TLEGGFYGPEGQBLGGKPLAHDKKVLYGFS 35							
Db	300 FVSDSDSLEGGFYGPQDGLGGKPLANDKKVLYAVS 335							
RESULT 11								
Q6H8W5	PRELIMINARY;	PRT;	593 AA.					
ID	Q6H8W5							

GN Name=tbpB;
 OS *Neisseria* *flavescens*.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC *Neisseriaceae*; *Neisseria*.
 NCBI_TaxID=484;
 RN [1] _TaxID=484;
 RP SEQUENCE FROM N.A.
 RC STRAIN=13120;
 RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
 RL EMBL; AT0704733; CAG28815.2; -;
 DR GO:0016020; C:membrane; IEA.
 DR GO:004998; P:transferrin receptor activity; IEA.
 DR InterPro; IPR001677; Transferrin_bind.
 DR Pfam; PF01298; Lipoprotein_5_1.
 SQ SSEQUENCE 594 AA; 64390 MW; P096DB939B046D0B CRC64;
 Query Match 73.4%; Score 136.5; DB 2; Length 594;
 Best Local Similarity 75.0%; Pred. No. 6.3e-10;
 Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;
 Qy 1 FTSEG-TLEGGFYGPQGLGGKPLAHDKVKLGVS 35
 Db 311 FVSDSDSLEGGFYGPQGLGGKPLAHDKVKLAVFS 346

RESULT 14

0533991 PRELIMINARY; PRT; 602 AA.
 AC 0533991; PRELIMINARY;
 DT 01-JUN-1998 (TREMBurel. 06, Created)
 DT 01-JUN-1998 (TREMBurel. 06, Last sequence update)
 DT 01-JUN-2003 (TREMBurel. 24, Last annotation update)
 DB TbpB precursor.
 GN Name=tbpB;
 OS *Neisseria meningitidis*.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC *Neisseriaceae*; *Neisseria*.
 NCBI_TaxID=487;
 RN [1] _TaxID=487;
 RP SEQUENCE FROM N.A.
 RC STRAIN=2713;
 MBLINE=38148004; PubMed=9479046; DOI=10.1016/S0378-1119(97)00646-X;
 RA Legrain M.; Robki B.; Villeval D.; Jacobs E.;
 RT "Characterization of genetic exchanges between various highly
 divergent *tbpB*, having occurred in *Neisseria meningitidis*."
 RL Gene 208:51-59 (1998).
 DR EMBL; AR223044; CAA11047.1; -;
 DR GO:0016020; C:membrane; IEA.
 DR GO:0004998; P:transferrin receptor activity; IEA.
 DR InterPro; IPR001677; Transferrin_bind.
 DR Pfam; PF01298; Lipoprotein_5_1.
 KW Signal.
 PT SIGNAL 1 20 Potential.
 SQ SSEQUENCE 602 AA; 65488 MW; 74641BP77B61C257 CRC64;
 Query Match 73.4%; Score 136.5; DB 2; Length 602;
 Best Local Similarity 75.0%; Pred. No. 6.4e-10;
 Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;
 Qy 1 FTSEG-TLEGGFYGPQGLGGKPLAHDKVKLGVS 35
 Db 320 FVSDSDSLEGGFYGPQGLGGKPLAHDKVKLAVFS 355

RESULT 15

Q6H8W0 PRELIMINARY; PRT; 594 AA.
 ID Q6H8W0
 AC Q6H8W0;
 DT 05-JUL-2004 (TREMBurel. 27, Created)
 DT 05-JUL-2004 (TREMBurel. 27, Last sequence update)
 DT 25-OCT-2004 (TREMBurel. 28, Last annotation update)

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Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	Alignments
Searched:	1612378 seqs, 512079187 residues		
Total number of hits satisfying chosen parameters:	1612378		
Minimum DB seq length:	0		
Maximum DB seq length:	2000000000		
Post-processing:	Minimum Match 0% Maximum Match 100%		
	Listing first 45 summaries		
Database :	UniProt_03: 1: uniprot_sprot: 2: uniprot_trembl:		
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	47	100.0 60 2 Q6DKQ8	Q6dkq8 neisseria m
2	47	100.0 410 2 Q6HB8U3	Q6hb8u3 neisseria m
3	47	100.0 526 2 Q71R42	Q71r42 haemophilus
4	47	100.0 545 2 Q71R38	Q71r38 haemophilus
5	47	100.0 547 2 Q44124	Q44124 actinobacil
6	47	100.0 547 2 Q44168	Q44168 actinobacil
7	47	100.0 547 2 Q44170	Q44170 actinobacil
8	47	100.0 560 2 Q71R40	Q71r40 haemophilus
9	47	100.0 566 2 Q6HB8U4	Q6hb8u4 neisseria m
10	47	100.0 567 2 Q6HB8U0	Q6hb8u0 neisseria m
11	47	100.0 569 2 Q6HB8T9	Q6hb8t9 neisseria m
12	47	100.0 569 2 Q6HB8U2	Q6hb8u2 neisseria m
13	47	100.0 570 2 Q6HB8U7	Q6hb8u7 neisseria m
14	47	100.0 571 2 Q6HB8U1	Q6hb8u1 neisseria m
15	47	100.0 572 2 Q6HB8U6	Q6hb8u6 neisseria m
16	47	100.0 573 2 Q6HB8T6	Q6hb8t6 neisseria m
17	47	100.0 579 2 Q6HB8T7	Q6hb8t7 neisseria m
18	47	100.0 579 2 Q9FC51	Q9fc51 neisseria m
19	47	100.0 582 2 Q9FC53	Q9fc53 neisseria m
20	47	100.0 586 2 Q9RDV1	Q9rdv1 neisseria m
21	47	100.0 593 2 Q44169	Q44169 actinobacil
22	47	100.0 593 2 Q6HB8V1	Q6hb8v1 neisseria s
23	47	100.0 593 2 Q6HB8W4	Q6hb8w4 neisseria f
24	47	100.0 593 2 Q6HB8W5	Q6hb8w5 neisseria c
25	47	100.0 593 2 Q6HB8W6	Q6hb8w6 neisseria s
26	47	100.0 594 2 Q6HB8V8	Q6hb8v8 neisseria m
27	47	100.0 594 2 Q6HB8W0	Q6hb8w0 neisseria f
28	47	100.0 594 2 Q6HB8W1	Q6hb8w1 neisseria f
29	47	100.0 594 2 Q6HB8W3	Q6hb8w3 neisseria f
30	47	100.0 596 2 Q71R44	Q71r44 actinobacil
31	47	100.0 596 2 Q83UA7	Q83ua7 actinobacil
RESULT 1			
ID	Q6DKQ8	PRELIMINARY;	PRT;
AC	Q6DKQ8;		60 AA.
DT	25-OCT-2004 (T-EMBLrel. 28, Created)		
DT	25-OCT-2004 (T-EMBLrel. 28, Last sequence update)		
DT	25-OCT-2004 (T-EMBLrel. 28, Last annotation update)		
DB	Transferin binding protein B (Fragment).		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;		
OC	Neisseriaceae; Neisseria.		
OX			
RN	[1] _TAXID=487;		
RP	SEQUENCE FROM N.A.		
RA	Trivedi S.;		
RL	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY660951; AAT13251; -.		
DR	Intertax; IPR001677; Transferrin_bind.		
DR	PFam: PF01298; Lipoprotein_5; 1.		
FT	NON_TER 1		
FT	NON_TER 60	60 AA;	6509 MW;
FT	SEQUENCE 60 AA;	6509 MW;	5A7424D75DFADCP4 CRC64;
RESULT 2			
ID	Q6HB8U3	PRELIMINARY;	PRT;
AC	Q6HB8U3;		410 AA.
DT	05-JUL-2004 (T-EMBLrel. 27, Created)		
DT	05-JUL-2004 (T-EMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (T-EMBLrel. 27, Last annotation update)		
DB	Transferin binding protein B (Fragment).		
GN	Name=tbpB;		
OS	Neisseria meningitidis.		
CC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;		
OC	Neisseriaceae; Neisseria.		
OX			
RN	[1] _TAXID=487;		
RP	SEQUENCE FROM N.A.		
RC	STRAN=Alpha3;		
RA	Harrison O.B.; Claus H.; Vogel U.; Bennett J.; Maiden M.; Rokbi B.;		
RL	EMBL; AJ704753; CAG88351; -.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0004998; F:transferrin receptor activity; IEA.		
DR	Intertax; IPR001677; Transferrin_bind.		

RESULT 13
 Q6HBT9 PRELIMINARY; PRT; 569 AA.
 ID Q6HBT9; PRELIMINARY; PRT; 569 AA.
 AC Q6HBT9; PRELIMINARY; PRT; 569 AA.
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Transferin binding protein B (Fragment).
 GN Name=tbpB;
 OS *Neisseria meningitidis*.
 OC Bacteria; Proteobacteria; Betaproteobacteria; *Neisseriales*;
 NCBI_TaxID=487;
 RN [1] _SEQUENCE FROM N.A.
 RC STRAIN=Alpha706;
 RA Harrison O.B.; Claus H.; Vogel U.; Bennett J.; Maiden M.; Rokbi B.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AU704757; CAG288393.1; -.
 GO; GO:0016020; C:membrane; IEA.
 DR GO:0004998; P:transferrin receptor activity; IEA.
 DR InterPro:IPR001677; Transferrin receptor activity; IEA.
 DR Pfam; PF01298; Lipoprotein_5; 1.
 FT NON TER 1
 FT NON TER 569 569
 SQ SEQUENCE 569 AA; 62323 MW; F7C31612B9152DEF CRC64;
 Query Match 100.0%; Score 47; DB 2; Length 569;
 Best Local Similarity 100.0%; Pred. No. 4.4%;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LEGGFYGP 8
 Db 288 LEGGFYGP 295

RESULT 12
 Q6HBW2 PRELIMINARY; PRT; 569 AA.
 ID Q6HBW2 PRELIMINARY; PRT; 569 AA.
 AC Q6HBW2 PRELIMINARY; PRT; 569 AA.
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 28, Last annotation update)
 DE Transferin binding protein B (Fragment) (Fragment).
 GN Name=tbpB;
 OS *Neisseria meningitidis*.
 OC Bacteria; Proteobacteria; Betaproteobacteria; *Neisseriales*;
 NCBI_TaxID=487;
 RN [1] _SEQUENCE FROM N.A.
 RC STRAIN=Alpha13;
 RA Harrison O.B.; Claus H.; Vogel U.; Bennett J.; Maiden M.; Rokbi B.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AU704755; CAG28837.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004998; P:transferrin receptor activity; IEA.
 DR InterPro:IPR001677; Transferrin receptor activity; IEA.
 DR Pfam; PF01298; Lipoprotein_5; 1.
 FT NON TER 1
 FT NON TER 569 569
 SQ SEQUENCE 569 AA; 62472 MW; GAFCE640D99DCA2F CRC64;
 Query Match 100.0%; Score 47; DB 2; Length 569;
 Best Local Similarity 100.0%; Pred. No. 4.4%;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LEGGFYGP 8
 Db 288 LEGGFYGP 295

RESULT 14
 Q6HBW1 PRELIMINARY; PRT; 571 AA.
 ID Q6HBW1 PRELIMINARY; PRT; 571 AA.
 AC Q6HBW1 PRELIMINARY; PRT; 571 AA.
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DE Transferin binding protein B (Fragment).
 GN Name=tbpB;
 OS *Neisseria meningitidis*.
 OC Bacteria; Proteobacteria; Betaproteobacteria; *Neisseriales*;
 NCBI_TaxID=487;
 RN [1] _SEQUENCE FROM N.A.
 RC STRAIN=Alpha13;
 RA Harrison O.B.; Claus H.; Vogel U.; Bennett J.; Maiden M.; Rokbi B.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AU704755; CAG28837.1; -.
 DR GO; GO:0004998; P:transferrin receptor activity; IEA.
 DR InterPro:IPR001677; Transferrin receptor activity; IEA.
 DR Pfam; PF01298; Lipoprotein_5; 1.
 FT NON TER 1
 FT NON TER 571 571
 SQ SEQUENCE 571 AA; 62265 MW; E3FDEB33921EC2D4 CRC64;
 Query Match 100.0%; Score 47; DB 2; Length 571;
 Best Local Similarity 100.0%; Pred. No. 4.4%;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q6HB06
 ID Q6HB06; PRELIMINARY; PRT; 572 AA.
 AC Q6HB06;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DB Transferrin binding protein B (Fragment).
 GN Name=rbpB;
 OS *Neisseria meningitidis*.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 NEisseriaceae; Neisseria.
 NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Alpha17;
 RA Harrison O.B., Claus H., Vogel U., Bennett J., Maidens M., Rokbi B.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ704750; CAG28832.1;
 DR GO; GO:0016020; C:membrane; IBA.
 DR GO; GO:0004998; F:transferrin receptor activity; IBA.
 DR InterPro; IPR01677; Transferrin_bind.
 DR Pfam; PF01298; Lipoprotein_5; 1.
 PT NON-TER 1 1
 PT NON-TER 572 572
 SQ SEQUENCE 572 AA; 62540 MW; 049BFD043ACBDOA CRC64;
 Query Match 100.0%; Score 47; DB 2; Length 572;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFTYGP 8
 Db 292 LEGGFTGP 299

Search completed: November 9, 2005, 19:16:35
 Job time : 33.4938 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 9, 2005, 18:43:14 ; Search time 31.6296 Seconds
(without alignments)

85.595 Million cell updates/sec

Title: US-10-043-344-85

Perfect score: 40

Sequence: 1 LEGGYFG 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dcc04:*

1: geneseqp19008:*

2: geneseqp19008:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20038:*

8: geneseqp20048:*

9: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	7	2 AAR77969	AAR77969 Antigenic
2	40	100.0	7	2 AAV46162	AAV46162 Predicted
3	40	100.0	7	2 AAY51767	AAY51767 H. influe
4	40	100.0	7	2 AAW54121	AAW54121 Tbp2 anti
5	40	100.0	7	2 AAW89426	AAW89426 Moraxella
6	40	100.0	7	3 AAY80464	AAY80464 H. influe
7	40	100.0	8	2 AAR77958	AAR77958 Antigenic
8	40	100.0	8	2 AAV46151	AAV46151 Predicted
9	40	100.0	8	2 AAV51756	AAV51756 H. influe
10	40	100.0	8	2 AAW54110	AAW54110 Tbp2 anti
11	40	100.0	8	3 AAY80453	AAY80453 H. influe
12	40	100.0	15	2 AAR77974	AAR77974 H. influe
13	40	100.0	15	2 AAV51789	AAV51789 H. influe
14	40	100.0	15	2 AAV54133	AAV54133 Polioviru
15	40	100.0	15	3 AAY80391	AAY80391 H. influe
16	40	100.0	16	2 AAR77973	AAR77973 H. influe
17	40	100.0	16	2 AAY51787	AAY51787 H. influe
18	40	100.0	16	2 AAY51788	AAY51788 H. influe
19	40	100.0	16	2 AAW54132	AAW54132 Polioviru
20	40	100.0	16	2 AAW54131	AAW54131 Polioviru
21	40	100.0	16	3 AAY80390	AAY80390 H. influe
22	40	100.0	16	3 AAY80389	AAY80389 H. influe
23	40	100.0	17	2 AAR77971	AAR77971 H. influe
24	40	100.0	17	2 AAY51786	AAY51786 H. influe
25	40	100.0	17	2 AAW54130	AAW54130 Polioviru

ALIGNMENTS

RESULT 1
AAR77969

ID AAR77969 standard; peptide; 7 AA.
XX
AC AAR77969;
XX DT 09-OCT-1996 (first entry)
XX DS Antigenic Tbp2 peptide Tbp2-36.
XX KW Tbp1; Tbp2; transferrin receptor operon; vaccine; antigen;
KW non-typable strain; Haemophilus influenzae; meningitis.
XX OS Synthetic.
XX PP 07-NOV-1994; 94WO-CA000616.
XX PN WO9513370-A1.
XX PD 18-MAY-1995.
XX PP 07-NOV-1994; 94WO-CA000616.
XX PR 08-NOV-1993; 93US-00148968.
XX PR 29-DEC-1993; 93US-00173116.
(CONN-) CONNAUGHT LAB LTD.
XX PI Loosmore S, Harkness R, Schryvers A, Chong P, Gray-Owen S;
PI Yang Y, Murdin A, Klein M;
XX DR WPI; 1995-19409/25.
XX DR WPI; 1995-19409/25.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	7	2 AAR77969	AAR77969 Antigenic
2	40	100.0	7	2 AAV46162	AAV46162 Predicted
3	40	100.0	7	2 AAY51767	AAY51767 H. influe
4	40	100.0	7	2 AAW54121	AAW54121 Tbp2 anti
5	40	100.0	7	2 AAW89426	AAW89426 Moraxella
6	40	100.0	7	3 AAY80464	AAY80464 H. influe
7	40	100.0	8	2 AAR77958	AAR77958 Antigenic
8	40	100.0	8	2 AAV46151	AAV46151 Predicted
9	40	100.0	8	2 AAV51756	AAV51756 H. influe
10	40	100.0	8	2 AAW54110	AAW54110 Tbp2 anti
11	40	100.0	8	3 AAY80453	AAY80453 H. influe
12	40	100.0	15	2 AAR77974	AAR77974 H. influe
13	40	100.0	15	2 AAV51789	AAV51789 H. influe
14	40	100.0	15	2 AAV54133	AAV54133 Polioviru
15	40	100.0	15	3 AAY80391	AAY80391 H. influe
16	40	100.0	16	2 AAR77973	AAR77973 H. influe
17	40	100.0	16	2 AAY51787	AAY51787 H. influe
18	40	100.0	16	2 AAY51788	AAY51788 H. influe
19	40	100.0	16	2 AAW54132	AAW54132 Polioviru
20	40	100.0	16	2 AAW54131	AAW54131 Polioviru
21	40	100.0	16	3 AAY80390	AAY80390 H. influe
22	40	100.0	16	3 AAY80389	AAY80389 H. influe
23	40	100.0	17	2 AAR77971	AAR77971 H. influe
24	40	100.0	17	2 AAY51786	AAY51786 H. influe
25	40	100.0	17	2 AAW54130	AAW54130 Polioviru

AAY80388 H. influe
Aar77934 Antigenic
Aaw46127 Predicted
Aay51732 H. influe
Aaw53087 Tbp2 anti
Aay80429 H. influe
Aar77945 Antigenic
Aaw46138 Predicted
Aay51743 H. influe
Aaw53098 Tbp2 anti
Aay80440 H. influe
Aay29819 Bacterici
Aaw43004 Truncated
Aay51809 H. influe
Aaw00504 N.meningi
Aar98887 N.meningi
Aaw14644 N. meningi
Aaw43005 Truncated
Aay51808 H. influe
Aaw43006 Truncated

Claim 11: Page 73; 231pp; English.

AAR77933-969 are predicted antigenic peptides derived from conserved regions of the Tbp2 protein from H. influenzae strains Bagat, Minna, DJ63 and non-typable strain PAK12085. The transferrin receptor (TFR) operon consists of two genes (Tbp1 and Tbp2) arranged in tandem and which are transcribed from a single promoter. H. influenzae TFR is iron- and/or haem-regulated and a putative fur-binding site has been identified upstream of Tbp2. Antibodies blocking this binding site may prevent bacterial growth. Fragments of the TFR (or its genes) are useful in vaccines to provide protection against, e.g. bacterial meningitis. An advantage of using the TFR is that it shares homology with TFR of other H. influenzae strains including non-typable strains. According to the

CC specification the present sequence shows residues 231-238 of Tbp2 from

CC the H. influenzae strain Eagan

XX Sequence 7 AA;

Query Match 100.0%; Score 40; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYG 7

Db 1 LEGGFYG 7

RESULT 2

AAW46162 ID AAW46162 standard; protein; 7 AA.

XX

AC AAW46162;

XX

DT 05-MAY-1998 (first entry)

XX

Predicted antigenic Tbp1 peptide TBP2-36.

XX

KW Transferrin receptor; Haemophilus influenzae type b; iron; human transferrin; iron source; antibody; bacterial growth; vaccine; immunogenic truncated analogue; antigen; Tbp1; Tbp2.

XX

KW immunogenic truncated analogue; antibody; Tbp1; Tbp2.

XX

OS Synthetic. Haemophilus influenzae.

XX

PN WO9640929-A2.

XX

PD 19-DEC-1996.

XX

PP 07-JUN-1996; 96WO-CA000399.

XX

PR 07-JUN-1995; 95US-004357.

XX

PR 17-JUN-1996; 96US-00639518.

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(CONN-) CONNAUGHT LAB LTD.

XX

PI Loosmore SM, Harkness RB, Schryvers AB, Chong P, Gray-Owen S, Yang Y; PI Murdin A, Klein M, Chong P;

XX

WPI: 1997-052329/05.

XX

Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used to induce protection against disease caused by transferrin producing pathogens, or as antigen to detect Haemophilus TFR antibodies.

XX

Example 16: Page 71; 228pp; English.

XX

Haemophilus truncated transferrin receptor protein derived from the Tbp2 protein of Haemophilus influenzae type b. Tbp2 is part of the transferrin receptor, of which Tbp1 is also a subunit. The deduced amino acid sequences of Tbp1 and Tbp2 were compared, and regions of conservation identified. The above peptides are derived from these regions, the present peptide being derived from residues 231-238. Iron is an essential nutrient for the growth of these bacteria, and they can utilise human transferrin as a source of iron. Antibodies which block the access of the transferrin receptor to its iron source prevent bacterial growth. The

CC candidates. An immunogenic composition comprising (or encoding) the

CC immunogenic truncated analogue can be used to induce protection against a

CC disease caused by a bacterial pathogen that produces the transferrin

CC receptor. The immunogenic truncated analogue is also useful as an antigen

CC in immunoassays for the detection of Haemophilus transferrin receptor

CC antibodies, while the nucleic acid molecule can be used as a

XX hybridisation probe for the detection of other transferrin receptor genes

Sequence 7 AA;

Query Match 100.0%; Score 40; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYG 7

Db 1 LEGGFYG 7

RESULT 3

AY51767 ID AAY51767 standard; protein; 7 AA.

XX

AC AAY51767;

XX

DT 13-JUN-2000 (first entry)

XX

DE H. influenzae antigenic Tbp2 peptide TBP2-36.

XX

KW Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine; diagnosis.

XX

OS Haemophilus influenzae.

XX

PN US6115688-A.

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PD 18-JAN-2000.

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PP 07-JUN-1995; 95US-00483577.

XX

PR 08-NOV-1993; 93US-00148968.

XX

PR 29-DEC-1993; 93US-00175116.

XX

PR 08-NOV-1994; 94US-00337483.

XX

PA (CONN-) CONNAUGHT LAB LTD.

XX

PI Loosmore S, Harkness R, Schryvers A, Gray-Owen S, Yang Y;

PI Murdin A, Klein M, Chong P;

XX

WPI: 1997-052329/05.

XX

Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used to induce protection against disease caused by transferrin producing pathogens, or as antigen to detect Haemophilus TFR antibodies.

XX

Example 16: Page 71; 228pp; English.

XX

AAW46162-62 are predicted antigenic peptides derived from the Tbp2 protein of Haemophilus influenzae type b. Tbp2 is part of the transferrin receptor, of which Tbp1 is also a subunit. The deduced amino acid

CC sequences of Tbp1 and Tbp2 were compared, and regions of conservation

CC identified. The above peptides are derived from these regions, the

CC present peptide being derived from residues 231-238. Iron is an essential

CC nutrient for the growth of these bacteria, and they can utilise human

CC transferrin as a source of iron. Antibodies which block the access of the

CC transferrin receptor to its iron source prevent bacterial growth. The

CC candidates. An immunogenic composition comprising (or encoding) the

CC immunogenic truncated analogue can be used to induce protection against a

CC disease caused by a bacterial pathogen that produces the transferrin

CC receptor. The immunogenic truncated analogue is also useful as an antigen

CC in immunoassays for the detection of Haemophilus transferrin receptor

CC antibodies, while the nucleic acid molecule can be used as a

XX hybridisation probe for the detection of other transferrin receptor genes

Sequence 7 AA;

Query Match 100.0%; Score 40; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYG 7

Db 1 LEGGFYG 7

RESULT 4

AY51767 ID AAY51767 standard; protein; 7 AA.

XX

AC AAY51767;

XX

DT 13-JUN-2000 (first entry)

XX

DE H. influenzae antigenic Tbp2 peptide TBP2-36.

XX

KW Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine; diagnosis.

XX

OS Haemophilus influenzae.

XX

PN US6115688-A.

XX

PD 18-JAN-2000.

XX

PP 07-JUN-1995; 95US-00483577.

XX

PR 08-NOV-1993; 93US-00148968.

XX

PR 29-DEC-1993; 93US-00175116.

XX

PR 08-NOV-1994; 94US-00337483.

XX

PA (CONN-) CONNAUGHT LAB LTD.

XX

PI Loosmore S, Harkness R, Schryvers A, Gray-Owen S, Yang Y;

PI Murdin A, Klein M, Chong P;

XX

WPI: 1997-052329/05.

XX

Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used

PT to induce protection against disease caused by transferrin producing

PT pathogens, or as antigen to detect Haemophilus TFR antibodies.

XX

Example 16: Page 71; 228pp; English.

XX

This invention describes a novel isolated and purified nucleic acid (I)

CC encoding an immunogenic, C-terminally truncated analog of one of the

CC transferrin receptor proteins Tbp1 or Tbp2 of Haemophilus influenzae

CC which has antibacterial activity. (I) are used for recombinant production

CC of truncated Tbp; as probes and primers for detecting, and diagnosing

CC infection by Haemophilus, also for isolating similar sequences from

CC other bacteria; as immunogens for vaccinating against infections caused

CC by bacteria that produce transferrin receptors, e.g. Haemophilus,

CC Neisseria or Brachamella. The truncated proteins are useful as immunogens

CC (as above); for diagnosing infection (as antigens in immunoassays) and

CC for raising antibodies, used for diagnosis of infections or for passive

CC immunization. AY51695 Y51767 represent H. influenzae

CC receptor proteins Tbp1 and Tbp2 antigenic peptide fragments

XX

Sequence 7 AA;

Query Match 100.0%; Score 40; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYG 7

Db 1 LEGGFYG 7

PT influenzae, useful for treating otitis media, epiglottitis, pneumonia and tracheobronchitis.
 XX Disclosure; Col 39-40; 252pp; English.
 CC The invention relates to novel antibodies (or monospecific antisera) specific for single transferrin receptor proteins (or immunogenic fragments) from strains of Haemophilus influenzae. This sequence corresponds to an epitope from the H. influenzae transferrin receptor protein Tbp2. The antibodies may be used for preventing and treating infections and disorders caused by H. influenzae, including bacterial meningitis, otitis media, epiglottitis, pneumonia and tracheobronchitis. The antibodies may also be used to detect the presence of H. influenzae proteins in samples according to standard methodologies (e.g. enzyme linked immunosorbent assay (ELISA)) and hence diagnose infections.

XX Sequence 7 AA;

Query Match 100.0%; Score 40; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LEGGYG 7
 Db 1 LEGGYG 7

XX RESULT 7

ID AAR77958 standard; peptide; 8 AA.
 XX AAR77958 standard; peptide; 8 AA.

AC AAR77958;

XX DT 09-OCT-1996 (first entry)

XX DE Antigenic Tbp2 peptide TBP2-25.

XX Tbp1; Tbp2; transferrin receptor operon; vaccine; antigen;
 KW non-typable strain; Haemophilus influenzae; meningitis.
 XX OS Synthetic.

XX PN WO95133370-A1.

XX PD 18-MAY-1995.

XX PF 07-NOV-1994; 94WO-CA000616.

XX PR 08-NOV-1993; 93US-00148968.

XX PR 29-DEC-1993; 93US-00175116.

XX PA (CONN-) CONNAUGHT LAB LTD.

XX DR 1995-194089/25.

XX PI Loosmore S, Harkness R, Schryvers A, Chong P, Gray-Owen S;
 PI Yang Y, Murdin A, Klein M;
 XX PS WPI; 1997-052329/05.

XX PT Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used to induce protection against disease caused by transferrin producing pathogens, or as antigen to detect Haemophilus Tfr antibodies.
 XX PS Example 16; Page 71; 228pp; English.
 XX CC AAM46126-62 are predicted antigenic peptides derived from the Tbp2 protein of Haemophilus influenzae type b. Tbp2 is part of the transferrin receptor, of which Tbp1 is also a subunit. The deduced amino acid sequences of Tbp1 and Tbp2 were compared, and regions of conservation identified. The above peptides are derived from these regions, the present peptide being derived from residues 231-238. Iron is an essential nutrient for the growth of these bacteria, and they can utilise human transferrin as a source of iron. Antibodies which block the access of the CC transferrin receptor, or fragments, therefore, are good vaccine candidates. An immunogenic composition comprising (or encoding) the CC immunogenic truncated analogue can be used to induce protection against a CC bacterial pathogen that produces the transferrin receptor. The immunogenic truncated analogue is also useful as an antigen CC in immunoassays for the detection of Haemophilus transferrin receptor CC antibodies, while the nucleic acid molecule can be used as a CC hybridisation probe for the detection of other transferrin receptor genes CC

XX advantage of using the Tfr is that it shares homology with Tfr of other H. influenzae strains including non-typable strains. According to the CC specification the present sequence shows residues 231-238 of Tbp2 from CC the H. influenzae strain Bagan.
 XX Sequence 8 AA;
 Query Match 100.0%; Score 40; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LEGGYG 7
 Db 1 LEGGYG 7

XX RESULT 8

ID AAM46151 standard; protein; 8 AA.
 XX AC AAM46151;
 XX DT 05-MAY-1998 (first entry)

XX DE Predicted antigenic Tbp1 peptide TBP2-25.
 KW Transferrin receptor; Haemophilus influenzae type b; iron;
 KW human transferrin; iron source; antibody; bacterial growth; vaccine;
 KW immunogenic truncated analogue; antigen; Tbp1; Tbp2.
 XX OS Synthetic.
 OS Haemophilus influenzae.

XX OS

XX PN WO9640929-A2.

XX XX PD 19-DEC-1996.

XX XX PP 07-JUN-1996; 96WO-CA000399.

XX XX PR 07-JUN-1995; 95US-00483577.

XX XX PR 17-MAY-1996; 96US-00649518.

XX XX PA (CONN-) CONNAUGHT LAB LTD.

XX XX PI Loosmore SM, Harkness RE, Schryvers AB, Chong P, Gray-Owen S;

XX XX PI Yang Y, Murdin AD, Klein M;

XX XX DR WPI; 1997-052329/05.

XX PT Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used to induce protection against disease caused by transferrin producing pathogens, or as antigen to detect Haemophilus Tfr antibodies.
 XX PS Example 16; Page 71; 228pp; English.
 XX CC AAM46126-62 are predicted antigenic peptides derived from the Tbp2 protein of Haemophilus influenzae type b. Tbp2 is part of the transferrin receptor, of which Tbp1 is also a subunit. The deduced amino acid sequences of Tbp1 and Tbp2 were compared, and regions of conservation identified. The above peptides are derived from these regions, the present peptide being derived from residues 231-238. Iron is an essential nutrient for the growth of these bacteria, and they can utilise human transferrin as a source of iron. Antibodies which block the access of the CC transferrin receptor, or fragments, therefore, are good vaccine candidates. An immunogenic composition comprising (or encoding) the CC immunogenic truncated analogue can be used to induce protection against a CC bacterial pathogen that produces the transferrin receptor. The immunogenic truncated analogue is also useful as an antigen CC in immunoassays for the detection of Haemophilus transferrin receptor CC antibodies, while the nucleic acid molecule can be used as a CC hybridisation probe for the detection of other transferrin receptor genes CC

XX AAR77933-969 are predicted antigenic peptides derived from conserved regions of the Tbp2 protein from H. influenzae strains Bagan, Mirm, DL63 and non-typable strain PA12085. The transferrin receptor (Tfr) operon consists of two genes (Tbp1 and Tbp2) arranged in tandem and which are transcribed from a single promoter. H. influenzae Tfr is iron- and/or haem-regulated and a putative fur-binding site has been identified upstream of tbp2. Antibodies blocking this binding site may prevent bacterial growth. Fragments of the Tfr (or its genes) are useful in vaccines to provide protection against, e.g. bacterial meningitis. An

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